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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model Run on:

October 1, 2004, 16:31:28

; Search time 55 Seconds (without alignments) 405.841 Million cell updates/sec

Title: Perfect sc Sequence:

US-09-841-091B-20 391 1 LELYQGIKFBASQKKSAKER.....NRIRSNSSAANLWAKKRVIR score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

genesequ1990s:* genesequ2000s:* genesequ2001s:* genesequ2001s:* genesequ2003as:* A_Geneseq_29Jan04:* 1: geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

ion	Human pep	Human CCK	Amino aci	Human cho	Human CCK	Enhanced	Sequence	LETO rat	Rat pancr	Rat pancr	Sequence	Guinea pi	Guinea pi		Guinea pi	Peptide #					Human bon	Human bra	Human liv	Peptide #	Human pep
Descript	Aaw29102	Aab66630	Abb99727	Abp81805	Abu62658	Aaw29104	Aar38890	Aaw21567	Aab66618	Abu62651	Aar40772	Aab66625	Abu62653	Aab66626	Abu62654	Aam15988	Abb34984	Aam28487	Abb29805	Abb20392	Aam68165	Aam55791	Abg49816	Aam03723	Abg37696
	9102	6630	9727	1805	2658	9104	8890	1567	6618	2651	0772	6625	2653	6626	2654	5988	4984	8487	9805	0392	8165	5791	9816	3723	ABG37696
CI .	AAWZ	AAB6	ABB9	ABP8	ABU6	AAW2	AAR3	AAW2	AAB6	ABU6	AAR4	AAB6	ABU6	AAB6	ABU6	AAM1	ABB3	AAM2	ABB2	ABB2	AAM6	AAMS	ABG4	AAMO	ABG3
8	N	4	9	φ	9	~	~	N	4	9	~	4	9	4	9	4	4	4	4	4	4	4	4	4	S
Length	428	428	428	428	428	428	444	444	444	444	430	430	430	450	450	176	176	176	176	176	176	176	176	176	176
Match	97.3	97.3	97.3	97.3	97.3	90.4	80.8	80.8	80.8	80.8	74.0	74.0	74.0	74.0	74.0	73.8			73.8	73.8				•	73.8
Score	380.5	380.5	380.5	380.5	380.5	353.5	316	316	316	316	289.5	289.5	289.5	289.5	289.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5	288.5
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Enhanc 380.8 444 2 AAW29104 Aaw29104 Enhanc 380.8 444 2 AAW29104 Aaw29104 Enhanc 380.8 444 2 AAW29104 Aaw21667 Aaw29104 Enhanc 380.8 444 2 AAW29104 Aaw21667 Aaw21667 Equinea 289.5 74.0 430 6 ABU62651 Aab6662 Guinea 289.5 74.0 430 6 ABU62653 Aaw26626 Guinea 289.5 74.0 430 6 ABU62654 Aaw26626 Guinea 289.5 74.0 450 6 ABU62654 Aaw15988 Peptid 380.5 73.8 176 4 AAW15988	Score Match Length DB ID 380.5 380.5 97.3 428 4 AAB66630 AAA29102 Human ADB99727 Amino ADB99727 Amino ADB91805 Human AAA29104 AAB66630 AAA29104 AAB66630 AAA29104 AAB66630 AAA29107 Amino AAA29107 Amino AAA29107 Amino AAA29107 Amino AAA29107 Amino AAA29107 Amino AAA399727 Amino AAA399972 Amino AAA3990 AAA3990 AAA3990 AAA3990 AAA6631 AAA6621 AAA66625 AAB6625 Guinea 289.5 74.0 74	Score Match Length DB ID Score Match Length DB ID SECORE MARCH COLOR AADS6630 Human CC SECORE MARCH COLOR AADS6630 Human CC SECORE MARCH COLOR AADS9104 MARCH COLOR AADS9105 Human CC SECORE MARCH COLOR AADS9104 MARCH COLOR AADS	Score Match Length DB ID 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This is the human peptide hormone cholecystokinin (hCCK) receptor A. A mutant form of this receptor can be created by substitution of certain

Disclosure; Page 54-55; 88pp; English.

the

Assay for peptide hormone receptor ligand using mutant forms of the receptors - where changes in second messenger signalling activity indicate that a compound is an agonist.

Ada09865 Human rec Ada09865 Human rec Ada70751 Human cho Ada79223 Human cho Ada79293 Human cho Ada70774 Sequence Ada73264 Human CCK Ada75778 Human CCK Ada75778 Human CCK Ada75778 Human CCK Ada80728 Human CCK Ada80728 Human CCK Adb99728 Amino aci Abb99728 Amino aci Abb99728 Amino aci	Human G prot Human Human
AAW21566 ADA09865 AAR80751 AAR802293 AAR40774 AAR40774 AAR57738 AAR57738 AAR57738 AAR57738 AAR6629 AAR83728 AB99728 AB99728	ADE83460 ABP82236 AAB02852 AAB02855 AAB02855
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1178 3386 3386 3386 3386 344444444444444444	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
000000000000000000000000000000000000000	28.6 27.4 27.1 27.1 26.9
	112 112 107 106 106
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. 4 4 4 4 4 5 4 6 6 4 6

ALIGNMENTS

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cholecystokinin; CCK; peptide hormone receptor; PHR; neuropeptide; mutant; messenger signal; agonist; antagonist; human; treatment; tumour; gastrointestinal disorder; central nervous system disorder; neurotoxin; substitution; enhanced receptor; hypoglyceamia.
                                                                                                                                                         /note= "Glu at this position can be substituted to Gln
(AAW29104)"
                                                                   Human peptide hormone cholecystokinin (CCK) receptor A.
                                                                                                                                                                                                                                                                                                   (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
                                                                                                                                               Location/Qualifiers
                AAW29102 standard; protein; 428 AA
                                                                                                                                                                                                                                                        96WO-US019958
                                                                                                                                                                                                                                                                       95US-00570157.
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                    Kopin AS, Beinborn M;
                                                                                                                                                                                                                                                                                                                                     WPI; 1997-332726/30.
                                                                                                                                                 Key
Misc-difference
                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                       11-DEC-1996;
                                                                                                                                                                                                                                                                         11-DEC-1995;
03-SEP-1996;
                                                                                                                                                                                                                      WO9721731-A1
                                                                                                                                                                                                                                      19-JUN-1997.
                                                    11-FEB-1998
                                 AAW29102;
RESULT 1
         AAW29102
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a minoacids (AAW29104). The mutant form of this receptor can be used in a a novel method for determining whether a candidate compound is an agonist or an antagonist of a peptide hormone receptor (FHR). The candidate compound is exposed to the mutant form of the PHR that has the ability to compound is exposed to the mutant form of the PHR that has the ability to amplify the activity of an agonist as compared to the corresponding wild-type receptor. A change in the second messenger signalling activity of the enhanced receptor can be measured to indicate whether the candidate compound is an agonist or an antagonist. The agonists and antagonists can be used for treating tumours, gastrointestinal disorders, central nervous system disorders in neuroleptic disorders; depression, schizophrenia, cisponse produced by chronic treatment or abuse of drugs or alcohol, cresponse produced by chronic treatment or abuse of drugs or alcohol, cresponse stroke, hypoglycaemia, cerebral palsy, spinal chord and head injury, poisoning by neurotoxins, infertility, adenomas, obesity or diabetes. The use of the mutant PHRs provides for the more sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholecystokinin (CCK) receptor-encoding DNA molecule, useful for lucing and purifying human CCK receptor protein to sequenceable-grade
                                                                                                                                                                                                                                                                                                                                                                                                LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                    Score 380.5; DB 2; Length 428; Pred. No. 6.9e-40;
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cholecystokinin; CCK receptor; purify.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 NRIRSNSSAANLMAKKRVIR 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB66630 standard; protein; 428
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92US-00861769.
92US-00928033.
92US-00937609.
                                                                                                                                                                                                                                                                                                                                  97.3%;
98.8%;
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90...
The 19; Conservative
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                                                                                                                                                                                                                                                                                                   Sequence 428 AA;
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The present invention relates to a cholecystokinin (CCK) receptor protein. The CCK receptor-encoding DNA molecule is useful for expressing and purifying CCK receptor protein to sequenceable-grade homogeneity. The

Disclosure; Fig 13; 82pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents human cholecystokinin-A (CCK-A) receptor. This receptor is a G protein-coupled receptor (GPCR) that is used to produce a single cell biosensor of the invention. The specification describes a single cell biosensor comprising a cell which overexpresses arrestin and at least one GPCR, where the GPCR, the arrestin or the cell is detectably labeled for monitoring internalisation of the GPCR. The biosensor detects various bioreactives, such as radioimmunoassay, which detects only the ligand species with the reactive epitope. The biosensor is useful for detecting a GPCR ligand in a test sample, for monitoring a GPCR ligand in a test sample, for continuous screening of GPCR ligands in a
CCK receptor proteins or fragments are useful for obtaining antibodies that can recognize CCK-expressing cells. The transformed eukaryotic cell lines are useful for studying the receptor in an environment similar to its native environment, e.g. in the context of studying the electrophysiology or binding properties of the receptor. The transformed prokaryotic or insect cell line is useful for expressing CCK receptor to produce large amounts of the receptor for immunological purposes or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel single cell biosensor, useful for detecting G protein-coupled receptor ligand in a sample, comprises cell overexpressing arrestin and protein-coupled receptor.
                                                                                                                                                                                                                                                                                             234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                            1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G protein-coupled receptor; GPCR; single cell biosensor; arrestin;
GPCR ligand; cholecystokinin-A receptor; CCK-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of human cholecystokinin-A (CCK-A) receptor.
                                                                                                                                                                                                                                          1,
                                                                                                                                                                                                      DB 4; Length 428;
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                studying protein structure, e.g. crystallography
                                                                                                                                                                                                    Score 380.5; DB 4
Pred. No. 6.9e-40;
0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oakley RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3F; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB99727 standard; protein; 428 AA
                                                                                                                                                                                                                                                                                                                                                                      294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                  60 NRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                      97.3%;
98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                          79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-140644/13.
N-PSDB; ABZ23129.
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Best Local Similarity
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                                                                                                                                                                    Sequence 428 AA;
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                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
ABB99727
     셤
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antibody against a particular GPCR, and in the production of specific

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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; ALDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atheroselerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular g protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                     5
                                                                                                                                                                                                           1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                    internalisation in a test sample. It is useful for altering GPCR internalisation. It is also useful for detecting an inhibitor of
                                                                                                                                                                         ;
  test sample, and for detecting a compound that modulates GPCR
                                                                                                                                   6; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cholecystokinin A receptor protein SEQ ID NO:94
                                                                                                                               97.3%; Score 380.5; DB 6;
98.8%; Pred. No. 6.9e-40;
iive 0; Mismatches 0;
                                                        acetylcholinesterase in a test sample
                                                                                                                                                                                                                                                                                                                                                                                                                             ABP81805 standard; protein; 428 AA
                                                                                                                                                                                                                                                                                                              Disclosure, Fig 1, 523pp, English.
                                                                                                                                                                                                                                                                                          NRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2001; 2001WO-US050107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burmer GC, Roush CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-046718/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune diseases.
                                                                                                                                                   Local Similarity
nes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABZ42651.
                                                                                            Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200261087-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002.
                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP81805;
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           ABP81805
                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                           8X33333
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antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for dagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, catherosclerosis, bacterial, fungal, protozoan or viral infections, osteodarthritis, osteodorosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, parkinson's disease, multiple sclerosis, graft, versus host of seed pression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42531 to ABZ42569 encode GPCR proteins given in ABPR91675 to ABPR82018, which are used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein, useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognize CCK-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                                                                                                       1,
                                                                                                                                                                                                                                                                                                                                                                                 97.3%; Score 380.5; DB 6; Length 428; 98.8%; Pred. No. 6.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; CCKB; cholecystokinin receptor; immunomodulator.
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                          exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU62658 standard; protein; 428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 NRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6; Fig 13; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-00861769.
92US-00928033.
92US-00937609.
93US-00029170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00443745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-00831248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CCKB receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-503641/47.
                                                                                                                                                                                                                                                                                                                                                Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACD26218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2003055238-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WANK/) WANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1992;
11-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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cholecystokinn (CCK) receptor protein. The invention also discloses a method for purifying a CCK receptor by solubilising a biological preparation containing CCK receptor in 1% digitionin, applying the solubilised receptor preparation to a cationic exchange resin and purifying the eluate of the resin. The purified eluate is then added to an agarcse-bound lectin and applied the eluate to a cibacron blue sepharose column and a CCK receptor protein of sequenceable-grade purity. The CCK receptor protein of the invention may have immunomodulatory activity. The DNA molecule of the invention is useful for purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK proteins are useful for neuroendocrine modulation of the immune system, and for sequence represents the human cholecystokinin (CCKB) receptor protein sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                    234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
                                                                                                                                                                                                                                                                                                                                                                             59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholecystokinin; CCK; peptide hormone receptor; PHR; neuropeptide; mutant; messenger signal; agonist; antagonist; human; treatment; tumour; gastrointestinal disorder; central nervous system disorder; neurotoxin; substitution; enhanced receptor; hypoglycaemia, MH21/35.
                                                                                                                                                                                                                                                                                                                                                                             1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                      Score 380.5; DB 6; Length 428;
Pred. No. 6.9e-40;
0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= M306A
/note= "wild type Met is replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= E1380
note= "wild type Glu is replaced by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "wild type Ala is replaced by His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "wild type Asn is replaced by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "wild type Leu is replaced by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enhanced CCK-A/gastrin receptor MH21/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW29104 standard; protein; 428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                            60 NRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= A303H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N304V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= L305S
                                                                                                                                                                                                                                                                                                    97.3%;
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96US-00718047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 98.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 305
                                                                                                                                                                                                                                                                        Sequence 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-1995;
03-SEP-1996;
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                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW29104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
AAW29104
ID AAW2
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This mutant CCK-A receptor M21/35 is derived from the human peptide

CC hormone cholecystokinin (hCCK) receptor A. This enhanced receptor MH21/35

CC is created by the substitution of wild type Glu to Gln at amino acid

CD position 138 and wild type Ala, Asn, Leu, Met to His, Val, Ser, Ala

CD Fe used in a novel method for determining whether a candidate compound is

CC andidate compound is exposed to the mutant form of the PHR that has the

CC andidate compound is exposed to the mutant form of the PHR that has the

CC candidate compound is exposed to the mutant form of the PHR that has the

CC andidate compound is exposed to the mutant form of the PHR that has the

CC carresponding wild-type receptor. A change in the second messenger

CC signalling activity of the enhanced receptor can be measured to indicate

Whether the candidate compound is an agonist or an antagonist. The

CS signalling activity of the enhanced for treating tumours, gastrointestinal

CC whether the candidate compound is an agonist or an antagonist. The

GODISTS and antagonists can be used for treating tumours, gastrointestinal

CC disorders, central hervous system disorders, neuroleptic disorders

CC disorders, withdrawal response produced by chronic treatment or

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, creatment or

Septinal chord and head injury, poisoning by neurotoxins, infertility,

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument or

Septinal chord and head injury, poisoning by neurotoxins, infertility,

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument or

Septinal chord and head injury, poisoning by neurotoxins, infertility,

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument or

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument or

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument or

CC abuse of drugs or alcohol, stress, stroke, hypoglycaemia, cateument

CC abuse of drugs or alcohol, stress, stroke, hypogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoded by the rat pancreatic cholecystokinin (CCK) A receptor cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                         Assay for peptide hormone receptor ligand using mutant forms of the receptors - where changes in second messenger signalling activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholecystokinin receptor protein; CCK; gastrointestinal receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.4%; Score 353.5; DB 2; Length 428; Best Local Similarity 93.8%; Pred. No. 2e-36; Matches 75; Conservative 0; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= glycosylation site
/note= "see also AAs 28,39,205"
                     (NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
                                                                                                                                                                                                      receptors - where changes in second mes
indicate that a compound is an agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR38890 standard; protein; 444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 NRIRSNSSAHVSAAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                               Claim 34; Page; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 NRIRSNSSAANLMAKKRVIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                        Beinborn M;
                                                                                                                      WPI; 1997-332726/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 428 AA;
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Modified-site
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07-FEB-1994
                                                                        Kopin AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR38890;
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The cholecystokinin (CCK)-A receptor gene of total length 10914 bp and coding for a protein having the present sequence was obtained from LETO rats and the sequences of all five exons, together with partial, flanking intron sequences were determined. Knowledge of the CCK-A receptor sequences is useful for genetic diagnosis of type II diabetes, e.g. by identifying a deleted site present in the CCK-A receptor gene of type II diabetes patients. Also, excession of CCK-A receptor mRNA is lowered or absent in the tissue of a cholelithiasis patient. (Updated on 17-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSR 308
                                                                                                                                                                                                      Genetic diagnosis of type II diabetes and cholelithiasis - by analysing cholecystokinin-A receptor expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 316; DB 2; Length 444;
Pred. No. 1.4e-31;
8; Mismatches 4; Indels
                                                                                                                                                                           N-PSDB; AAT71575, AAT71576, AAT71577, AAT71579, AAT71579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cholecystokinin; CCK receptor; purify
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat pancreatic CCKA receptor protein.
                                                                                                                                                                                                                                            Disclosure; Page 6-9; 13pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 LNRIRSSSSAANLIAKKRVIR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 ANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB66618 standard; protein; 444
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92US-00861769.
92US-00928033.
92US-00937609.
                                                                                                                95JP-00178234.
                                                                                         95JP-00353546.
                                                                                                                                                                                                                                                                                                                                                                                                                      80.8%;
82.7%;
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                                                                                                                                                                  WPI; 1997-220430/20
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Best Local Similarity
               Rattus sp; (LETO).
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 444 AA;
                                       JP09065900-A.
                                                                                         29-DEC-1995;
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11-AUG-1992;
02-SEP-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated DNA molecule encoding cholecystokinin receptor protein - are purified to isolate cholecystokinin receptor clones and produce anticholecystokinin receptor antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diabetes mellitus, type 2 diabetes, CCK-A receptor, cholelithiasis, gallstone, diagnosis, deletion, mutation, LETO rat, OLETF rat, Otsuka Long-Evans Tokushima Fatty.
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82.7%; Pred. No. 1.4e-31;
ive 8; Mismatches 4; Indels
                                                 131. .152
/label= transmembrane III
173. .193
                                                                                                                                     /label= transmembrane VI
366. 389
/label= transmembrane VII
                        93. .119
/label= transmembrane II
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              transmembrane 1
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92US-00861769.
92US-00928033.
92US-00937609.
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(first entry)
                                                                                                                            330. .350
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Best Local Similarity 82.7
Matches 67; Conservative
 57. .82
/label=
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06-AUG-1997
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note= "Asn is N-glycosylated"

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                                                                                                                                                              The present invention relates to a cholecystokinin (CCK) receptor protein. The CCK receptor-encoding DNA molecule is useful for expressing and purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK receptor proteins or fragments are useful for obtaining antibodies that can recognize CCK-expressing cells. The transformed eukaryotic cell lines are useful for studying the receptor in an environment similar to its native environment, e.g. in the context of studying the electrophysiology or binding properties of the receptor. The transformed produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for t
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                                                                New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for producing and purifying human CCK receptor protein to sequenceable-grade
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; CCKA; cholecystokinin receptor; immunomodulator; receptor.
                                                                                                                                                                                                                                                                                                                                                                                              Score 316; DB 4; Length 444;
Pred. No. 1.4e-31;
8; Mismatches 4; Indels
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132. .158
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/note= "Transmembrane domain IV"
205
                                                                                                                                                                                                                                                                                                                                     studying protein structure, e.g. crystallography
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat pancreatic CCKA receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU62651 standard; protein; 444 AA
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                                                                                                                                  Disclosure; Fig 1; 82pp; English
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Matches 67; Conservative
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/note= "1
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                               WPI; 2001-136725/14.
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cholecystokinin (CCK) receptor protein. The invention also discloses a method for purifying a CCK receptor by solubilising a biological preparation containing CCK receptor in # digitonin, applying the solubilised receptor preparation to a cationic exchange resin and purifying the eluate of the resin. The purified eluate is then added to an agarose-bound lectin and applied the eluate to a cibacron blue sepharose column and a CCK receptor protein of sequenceable-grade purity. The DNA molecule of the invention may have immunomodulatory activity. The DNA molecule of the invention is useful for purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK proteins are useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognise CCK-expressing cells. The present sequence represents the rat cholecystokinin (CCKA) receptor protein of
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                                                                                                                                                                       cleavage
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                                                                                   'note= "Peptide fragment obtained by CNBr
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82.7%; Pred. No. 1.4e-31;
ive 8; Mismatches 4.
                          "Transmembrane domain V"
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nes 67; Conservative
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N-PSDB; ACD62651.
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01-APR-1992;
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                                                                    Sequence encoded by the cholecystokinin (CCK) A receptor cDNA in guinea pig gallbladder and pancreas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The rat pancreatic CCK A receptor cDNA clone encodes a protein with transmembrane domains, and homology with other G-protein receptor superfamily members. There are 4 potential sites of N-linked glycosylation and sites for serine and threonine phosphorylation. (Updated on 25-WAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                 /label= Phosphorylation
/note= "see also AAs 256,274,292,300,414,416,419"
                                                                                            Cholecystokinin receptor protein; CCK; gastrointestinal receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.0%; Score 289.5; DB 2; Length 430;
                                                                                                                                           /label= glycosylation
/note= "see also AAs 12,24,190"
                                                                                                                                                          44. .67
/label= transmembrane domain I
                                                                                                                                                                                                                                                                                                         /label= phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICE
                                                                                                                     Location/Qualifiers
10
              AAR40772 standard; protein; 430 AA.
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92US-00861769.
92US-00928033.
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                                                                                                                                                                            80. .103
/label= II
118. .137
/label= III
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/label= VII
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                                                                                                                                                                                                           158. .179
/label= IV
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/label= VI
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/label= V
                                              (revised)
(first entry)
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N-PSDB; AAQ47669.
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                                                                                                            Cavia porcellus
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11-AUG-1992;
02-SEP-1992;
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                                              25-MAR-2003
07-FEB-1994
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                               AAR40772;
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RESULT 11
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                                                                                                                     234 LELYQCIKFDAIQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPRKLELRQLSPSSGGSN 293
                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for producing and purifying human CCK receptor protein to sequenceable-grade
                                                                                  1 LELYQCIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS
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                             Gaps
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                             Indels
                          10;
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79.3%; Pred. No. 3.3e-28;
tive 4; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cholecystokinin, CCK receptor; purify.
                                                                                                                                                                                                                               294 RINRIRSSSSTANLMAKKRVIR 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suinea pig CCKA receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                AAB66625 standard; protein; 430
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                                                                                                                                                                                              58 RANRIRSNSSAANLMAKKRVIR
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92US-00861769.
92US-00928033.
92US-00937609.
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Best Local Similarity 79.3
Matches 65; Conservative
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Best Local Similarity
Matches 65; Conserv
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Query Match

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This invention relates to a novel isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein. The invention also discloses a method for purifying a CCK receptor by solubilising a biological preparation containing a CK receptor in 1% digitonin, applying the solubilised receptor preparation to a cationic exchange resin and publised receptor preparation to a cationic exchange resin and a cationic purifying the eluate of the reain. The purified eluate is then added to an agarose-bound lectin and applied the eluate to a cibacron blue sepharose column and a CCK receptor protein of sequenceable-grade homogeneity. The CCK proteins are cuseful for neuroendocrine modulation of the immune system, and for useful for neuroendocrine modulation of the immune system, and for sequence represents the guinea pig cholecystokinin (CCKA) receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
                                                                                          New isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein, useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognize CCK-expressing cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.0%; Score 289.5; DB 6
79.3%; Pred. No. 3.3e-28;
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                                                                                                                                                                     Example 3; Fig 6; 83pp; English
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92US-00861769.
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                                        2003-503641/47.
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Best Local Similarity
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                                                     N-PSDB; ACD26215
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01-APR-1992;
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   Wank SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Serine phosphorylation site"
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158. .179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Transmembrane domain II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Transmembrane domain I"
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/note= "Transmembrane domain V"
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/note= "Transmembrane domain V"
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/note= "Transmembrane domain V"
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                                                                                                                                                                                                                                                                                                              Location/Qualifiers
294 RINRIRSSSSTANLMAKKRVIR 315
                                                                                        ABU62653 standard; protein; 430 AA.
                                                                                                                                                                                                    Guinea pig CCKA receptor protein.
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92US-00861769.
92US-00928033.
92US-00937609.
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Gaps 3;

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Length 430;

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                                                              The present invention relates to a cholecystokinin (CCK) receptor and purifying CCK receptor protein to sequenceable-grade homogeneity. The CCK receptor protein to sequenceable-grade homogeneity. The CCK receptor proteins or fragments are useful for obtaining antibodies that can recognize CCK-expressing cells. The transformed eukaryotic cell lines are useful for studying the receptor in an environment similar to its native environment, e.g. in the context of studying the electrophysiology or binding properties of the receptor. The transformed produce large amounts of the receptor for immunological purposes or for produce large amounts of the receptor for immunological purposes or for
                                                                                                                                                                                                                                                                               New cholecystokinin (CCK) receptor-encoding DNA molecule, useful for producing and purifying human CCK receptor protein to sequenceable-grade
                                                                                                                                                                                                                                                                  1 LELYQGIKFBASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS
                                                                                                                                                                                                                                            3; Gaps
                                                                                                                                                                                                                     74.0%; Score 289.5; DB 4; Length 450; 79.3%; Pred. No. 3.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guinea pig; CCKA; cholecystokinin receptor; immunomodulator.
                                                                                                                                                                                                                                            4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Transmembrane domain III
                                                                                                                                                                             studying protein structure, e.g. crystallography
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Transmembrane domain I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guinea pig CCKA receptor protein #2.
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                             58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                       ABU62654 standard; protein; 450 AA
                                           Disclosure; Fig 7; 82pp; English.
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92US-00861769.
92US-00928033.
92US-00937609.
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Matches 65; Conservative
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01-APR-1992;
11-AUG-1992;
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Domain
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cholecystokinin (CCK) receptor protein. The invention also discloses a method for purifying a CCK receptor by solubilising a biological preparation containing CCK receptor in 14 digitonin, applying the solubilised receptor preparation to a cattonic exchange resin and purifying the eluate of the resin. The purified eluate is then added to an agarose-bound lectin and applied the eluate to a cibacron blue sephazose column and a CCK receptor protein of sequenceable-grade purity. The CCK receptor protein of the invention may have immunomodulatory activity. The DNA molecule of the invention is useful for purifying CCK receptor protein of the invention is useful for purifying CCK receptor protein of the invention of the immune system, and for obtaining antibodies that can recognise CCK-expressing cells. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
                                                                                                                                                                                                                                                                                        New isolated DNA molecule encoding a cholecystokinin (CCK) receptor protein, useful for neuroendocrine modulation of the immune system, and for obtaining antibodies that can recognize CCK-expressing cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents the guinea pig cholecystokinin (CCKA) receptor protein sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel isolated DNA molecule encoding
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79.3%; Pred. No. 3.5e-28;
live 4; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 7; 83pp; English.
93US-00029170
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                                                                        (WANK/) WANK S A.
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Best Local Similarity 98.8%;
Matches 79; Conservative
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MOLECULE TYPE: protein
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STATE: MA
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-029-170-14
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 5780, Ap
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Patent No. 5750353
GENERAL INFORMATION:
APPLICANT: Reinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS; NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIP: 02110-2804

COUNTRY: USA

COMPUTER READBLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/570,157

FILING DATE: 11-DEC-1995

CLASSIFICATION: 435

ATYONEY/AGENT INPORMATION:

NAME: CLARK, Paul T:

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 30,162

TELEPRAK: 617/442-8906

TELEPRAK: 617/542-8906
                                  US-08-029-170-16
US-08-570-157-2
US-09-076-510-2
US-09-004-349-2
US-07-978-892A-5
US-08-570-157-4
US-08-570-157-4
US-09-076-510-4
US-09-05-134-000C-5780
US-08-930-894-5
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STRANDEDNESS: not relevant
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Length 428; Indela

Score 380.5; DB 1; Pred. No. 3.2e-39; 0; Mismatches 0;

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                                                                                                                                                                         US-08-029-170-31
Sequence 31, Application US/08029170
Sequence 31, Application US/08029170
Settle No. 6169173
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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ZIPE: 22313-029
COUNTRY: USA
ZIP: 22313-029
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/029,170
CLASSIFCATION NUMBER: US/08/029,170
FLING DATE: 19930310
CLASSIFCATION NUMBER: US 07/937,609
FRIDRA APPLICATION DATA:
APPLICATION NUMBER: US 07/937,609
FRIDRA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
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Pred. No. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
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                                     294 NRIRSNSSAANLMAKKRVIR 313
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60 NRIRSNSSAANLMAKKRVIR 79
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INFORMATION FOR SEQ ID NO: 31:
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Best Local Similarity 98.8
Matches 79; Conservative
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RESULT 3

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GENERAL INFORMATION:
APPLICANT: KOpin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR AND USES OF PEPTIDE HORMONE
TITLE OF INVENTION: RECEPTOR AGONISTS
FILE REPERENCE: 00399/11002
CURRENT APPLICATION NUMBER: US/09/004,349A
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: 08/570,157
EARLIER FILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 23
                                            GENERAL INFORMATION:

APPLICANT: KOPIN, Alan S.

APPLICANT: Beinborn, Martin

TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO

TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSES: Clark & Blbing LLP

STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.3%; Score 380.5; DB 4
98.8%; Pred. No. 3.2e-39;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,510
FILING DATE: 12 MAY 1998
PRIOR APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
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Sequence 5, Application US/09076510
Patent No. 6376198
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LENGTH: 428 amino acids
TYPE: amino acid
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Best Local Similarity 98.8
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TELEFAX: 617/438-7045
TELEX:
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; MOLECULE TYPE: protein
US-09-076-510-5
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                     CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02110
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308 LNRIRSSSSAANLIAKKRVIR 328
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                                                                                                                                              97.3%; Score 380.5; DB 4; Length 428;
llarity 98.8%; Pred. No. 3.2e-39;
Conservative 0; Mismatches 0; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08570157
Patent No. 5750353
GENERAL INFORMATION. Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: AADDRESSE: Fish & Richardson P.C.
STREET: 225 Pranklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,157
FLING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMMS: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
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TELECOMMUTCATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                    294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 ANRIRSNSSAANLMAKKRVIR 79
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Conservative
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                                                                               ; ORGANISM: Homo sapiens
US-09-004-349-5
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                                                                                                                                              Query Match
Best Local Similarity
Matches 79; Conserv
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                                                             TYPE: PRT
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                                           LENGTH
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248 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSR 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.8%; Score 316; DB 4; Length 443; Best Local Similarity 82.7%; Pred. No. 3.6e-31; Matches 67; Conservative 8; Mismatches 4; Indels
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Patent No. 6566080
GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR AND USES OF PEPTIDE HORMONE
TITLE OF INVENTION: RECEPTOR AGONISTS
FILE REFERENCE: 00398/118002
CURRENT APPLICATION NUMBER: US/09/004,349A
                                                                                     APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/076,510
FILING DATE: 12 MAY 1998
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US-09-076-510-6; Sequence 6, Application US/09076510; Patent No. 6376198
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176 Federal Street
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,1
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 443 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                             STREET: 176 FCITY: Boston
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                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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US-09-004-349-6
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TOPOLOGY:
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Patent No. 2319073
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLLY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSET APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FILING DATE: 19920902
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-PEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION:
TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
CURRENT FILING DATE: 1998-01-08
EARLIER APPLICATION NUMBER: 08/570,157
EARLIER FILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 LNRIRSSSSAANLIAKKRVIR 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 4444 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Rattus norvegicus
US-09-004-349-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-07-937-609-14
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US-07-937-609-14
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                                                                                                                                                                                                                                                       CENGTH: 443
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1 LELYQGIKFEASQXKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR 58
                                                                                                                1 LBLYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                               Gaps
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Score 316; DB 1; Length 444; Pred. No. 3.6e-31; 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
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OPERATION OF THE CLOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,170
FILING DATE: 19930310
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: US 07/861,769
FILING DATE: US 07/861,769
FILING DATE: US 07/861,769
FILING DATE: US 07/81,248
FILING DATE: US 07/81,248
FILING NUMBER: US 07/831,248
FREFERENCE/MOUNING NUMBER: US 07/831,248
FREFERENCE/MOUNING NUMBER: US 07/831,248
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80.8%; Score 316; DB 3;
Best Local Similarity 82.7%; Pred. No. 3.6e-31;
Matches 67; Conservative 8; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
COUNTRY: USA
ZIP. 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              309 LNRIRSSSSAANLIAKKKVIR 329
                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-029-170-14
; Sequence 14, Application US/08029170
; Patent No. 6169173
                                                                                                                                                                                                                                            59 ANRIRSNSSAANLMAKKRVIR 79
            80.8%;
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TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                  67; Conservative
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            Query Match
Best Local Similarity
Matches 67; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 430;
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CLOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: USA

ZIP: 22313-0299
COUNTY: USA
ZIP: 22313-0299
COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHILIN RClease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/937,609
FLING DATE: 19920902
CLASSIFCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FLING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FLING DATE: 01-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 1010199/166 NIHD
TELECOMMUNICATION INFORMATION:
MUTUAL PROPERTION:
TELECOMMUNICATION INFORMATION:
TOTAL PROPERTION:
TOTAL PROPERTION NUMBER: 29,768
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79.3%; Pred. No. 6.9e
tive 4; Mismatches
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                                                                         309 LNRIRSSSSAANLIAKKRVIR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 RANRIRSNSSAANLMAKKRVIR 79
                                                59 ANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                 ; Sequence 23, Application US/07937609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 430 amir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 79.3
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-07-937-609-23
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US-08-919-624-3
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234 LELYQGIKFDAIQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPRKLELRQLSPSSSGSN 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
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Patent No. 6169173
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Guegler, Karl J.
APPLICANT: CORLEY, Neil C.
TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 289.5; DB 2;
Pred. No. 6.9e-28;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: 164 Computer:
COMPUTER: 164 Computer:
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,624
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: FILED HERWITH
PRIOR APPLICATION NUMBER:
FILING DATE:
FILING
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Best Local Similarity 79.3
Matches 65; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: si
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-029-170-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
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Pred. No. 7.3e-28;
4; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poley & Lardner
STERES: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/029,170
FILING DATE: 19930310
CLASSIFICATION 7435
PRIOR APPLICATION PARER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
                                              PION BAPLICATION: 436
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INPOMBER: US 07/928,033
ATTORNEY/AGENT INPOMBER: US 07/928,033
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 RINRIRSSSTANLWAKKRVIR 335
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ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: guinea pig CCKA receptor
US-07-937-609-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 24, Application US/08029170 Patent No. 6169173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 450 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.0
Best Local Similarity 79.3
Matches 65; Conservative
   FILING DATE: 19
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/07937609

Retent No. 5313073

GENERAL INFORMATION:

APPLICANT: WANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF

TITLE OF INVENTION: CLOLECYSTOKININ RECEPTOR-ENCODING DNA

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLLY & Lardner

STREET: 1800 Diagonal Road, Suite 500

CONTY: ALACANDATION

CITY: ALACANDATION

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/029,170
FILING DATE: 19930310
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.0%; Score 289.5; DB 3
79.3%; Pred. No. 6.9e-28;
                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-58P-1992
PRIOR APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATORREY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET UNMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 RINRIRSSSTANLMAKKRVIR 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LEWIGH: 430 ami-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 79.3
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-029-170-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-570-157.

15. Sequence 7, Application US/08570157

16. Patent No. 5750353

17. General Information;

18. APPLICANT: Robin, Alan S.

18. APPLICANT: Beinborn, Martin

18. TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS

18. TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS

18. TITLE OF INVENTION: PEPTIDE HORMONE RECEPTORS

18. CORRESPONDENCES 13.

18. COUNTRY: USA

18. COUNTRY: USA

18. COMPUTER READABLE FORM:

18. MEDIUM TYPE: Ploppy disk

19. COMPUTER: IBM PC compatible

19. OPERATION NUMBER: DC-005/MS-DOS

20. COMPUTER: IBM PC compatible

20. COMPUTER: IBM PC compatible

30. COMPUTER: LI-DEC-1995

30. CURRENT APPLICATION DATA: A15

51. TILLIG DATE: 11-DEC-1995

52. CLASSIFICATION NUMBER: 30,162

53. REFERENCE/DOCKET NUMBER: 30,162

54. REFERENCE/DOCKET NUMBER: 30,162

55. RELEPHONE: 617/542-8906

56. TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.0%; Score 289.5; DB 3
Best Local Similarity 79.3%; Pred. No. 7.3e-28;
Matches 65; Conservative 4; Mismatches 10
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENTY Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 RINRIRSSSSTANLWAKKRVIR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; IMMEDIATE SOURCE:
; CLONE: guinea pig CCKA receptor
US-08-029-170-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-570-157-7
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A. 15

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TYPE: amino acid

| TYPE: Amino acid
| STRANDEDBESS: not relevant
| TOPOLOGY: linear
| TO
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13

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October 1, 2004, 16:37:50 ; Search time 130 Seconds (without alignments) 195.555 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                       1 LELYQGIKFEASQKKSAKER......NRIRSNSSAANLMAKKRVIR 79
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PUS06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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prodata/2/pubpa/US09C_PUBCOMB_pep:
prodata/2/pubpaa/US09C_PUBCOMB_pep:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1351062 segs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                    US-09-841-091B-20
391
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                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	
Result No.	Score	% Query Match	% Query Match Length DB	DB	ΩI	Description
	1 1 1 1 1 1 1 1	1		-		
- -1	391	100.0	79	12	US-09-841-091B-20	Sequence 20, Appl
7	391	100.0		14	US-10-251-703-20	Sequence 20, Appl
М	380.5	97.3	428	10	US-09-443-745-31	Sequence 31, Appl
4	380.5	97.3	428	14	US-10-225-567A-94	Sequence 94, Appl
r.	380.5	97.3		14	US-10-060-369-12	Sequence 12, Appl
9	380.5	97.3		14	US-10-127-940-5	2
7	380.5	97.3		14	US-10-441-757-5	s,
60	316	80.8		14	US-10-127-940-6	Sequence 6, Appli
o,	316	80.8		14	US-10-441-757-6	Sequence 6, Appli
10	316	80.8		10	US-09-443-745-14	Sequence 14, Appl
11	289.5	74.0		10	US-09-443-745-23	Sequence 23, Appl
12	289.5	74.0		10	US-09-443-745-24	Sequence 24, Appl
13	288.5	73.8	176	σ	US-09-864-761-35690	Sequence 35690, A
14	151	38.6	453	14	US-10-127-940-7	Sequence 7, Appli

Sequence 7, Appli

14 US-10-441-757-7

453

38.6

151

12

equence 1 equence 2 equence 2 equence 1 equence 2 equence 3 equence 3 equence 3 equence 3 equence 6 equence 1 equence 1 equence 1 equence 1 equence 1 equence 2 equence 3	11 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
09-841-091B-1 09-443-745-29 10-1576-255-27-1 10-225-567A-1 10-417-820A-7 10-417-820A-7 10-417-820A-1 10-425-567A-3 10-417-820A-1 10-	US-09-841-091B-13 US-10-251-703-13 US-09-443-745-27 US-10-127-940-4 US-10-441-757-4 US-09-841-091B-14 US-10-251-703-14
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11111222222222222222222222222222222222	W 4 4 4 4 4 9 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0

ALIGNMENTS

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Sequence 20, Application US/09841091B
; Publication No. US20020076755A1
; GENERAL INFORMATION:
; APPLICANT: Kuliopulos, Athan
; APPLICANT: Kuliopulos, Athan
; APPLICANT: Covic, Lidija
; TITLE OF INVENTION: G Protein Coupled Receptor (GPCR) Agonists and TITLE OF INVENTION: GPCR Using the Same
; FILE REPERENCE: 18475-034
; CURRENT APPLICATION NUMBER: US/09/841,091B
; CURRENT APPLICATION NUMBER: 60/198,993
; PRIOR FILING DATE: 2000-04-21
; NUMBER: OF SEQ ID NOS: 29
; SOFTWARE: PATENTIN VEY: 2.1
; SEQ ID NO 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LELYQGIKPEASQKKSAKERKPSTTSSGKYEDSDGCYLKTRPPRKLELRQLSTGSSSRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Pepducin; OTHER INFORMATION: Peptide Sequence
US-09-841-091B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 391; DB 12; Best Local Similarity 100.0%; Pred. No. 1e-37; Matches 79; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RIRSNSSAANLMAKKRVIR 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
JS-09-841-091B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 79; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                             APPLICANT: Kuliopulos, Athan
APPLICANT: Covic, Lidija
APPLICANT: Covic, Lidija
TITLE OF INVENTION: G Protein Coupled Receptor Agonists and TITLE OF INVENTION: G Protein Coupled
TITLE OF INVENTION: Receptors Using the Same
FILE REPERENCE: NEMC-21s CIP
CURRENT APPLICATION NUMBER: US/10/251,703
CURRENT FILING DATE: 2002-09-20
PRIOR FILING DATE: 2001-04-23
PRIOR FILING DATE: 2000-04-21
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 20
LENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLKTRPPRKLELRQLSTGSSSRAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLKTRPPRKLELRQLSTGSSSRAN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 391; DB 14; Length 79; 100.0%; Pred. No. 1e-37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/09443745
Publication No. US20030055238A1
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLLY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence; ; OTHER INFORMATION: Peptide Sequence
US-10-251-703-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/443,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
                    ; Sequence 20, Application US/10251703; Publication No. US20030148449A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.v
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US-10-251-703-20
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US-09-443-745-31
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Licespan Biosciences
APPLICANT: Burmer, Glenna C.
APPLICANT: Rouse, Christine L.
APPLICANT: ROUSEL 1920-4-4
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: 0210/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR PRIOR APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER: OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 94
LENGTH 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.3%; Score 380.5; DB 14; Lengua
98.8%; Pred. No. 1.3e-35;
wismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 380.5; DB 1
Pred. No. 1.3e-35;
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/831,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INPORMATION:
NAME: BENTY, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 NRIRSNSSAANLMAKKRVIR 313
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                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.3%;
98.8%;
                                                                                                                                                                                                                                                                                                       TELEPHONE: (703,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79; Conservative
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-10-127-940-6
                                                                                                                                          US-10-127-940-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Score 380.5; DB 14; Length 428;
Pred. No. 1.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kopin, Alan S.
Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
PEPTIDE HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                             Sequence 12, Application US/10060369
Publication No. US20030139589A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR A4
FILE REFERENCE: 2931-104
CURRENT APPLICATION NUMBER: US/10/060,369
CURRENT APPLICATION NUMBER: US 09/173565
FRIOR APPLICATION NUMBER: US 09/173565
NUMBER OF SEQ ID NOS: 12
SOFTWARE PATENTY DATE: 1998-08-16
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/109002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: U5/09/076,510
FILING DATE: 12 MAY 1998
APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
ATTOWNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,940
FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SEARTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PastSeq version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
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INFORMATION FOR SEQ ID NO: 5:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                    US-10-060-369-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-127-940-5
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234 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRA 293
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Sequence 5, Application US/10441757

Publication No. US2003019111441

GENERAL INPORMATION:
APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: RECEPTOR AGONISTS

FILE OF INVENTION: RECEPTOR AGONISTS

FILE REFERENCE: 00398/118002

CURRENT APPLICATION NUMBER: US/10/441,757

CURRENT PLING DATE: 1998-01-08

PRIOR PELING DATE: 1998-01-08

PRIOR PELING DATE: 1998-12-11

NUMBER OF SEQ IN NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10127940
Publication No. US20030180798A1
GENERAL INFORMATION:
APPLICANT: Kopin, Alan S.
Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
PEPTIDE HORMONE RECEPTORS
                                                                                                                                                                                                                   Query Match
97.3%; Score 380.5; DB 14; Length
Best Local Similarity 98.8%; Pred. No. 1.3e-35;
Matches 79; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                       TYPE: amino acid
STRANDEDNESS: No. US20030180798A1 Relevant
TOPOLOCY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.3%; Score 380.5; DB 14;
98.8%; Pred. No. 1.3e-35;
Live 0; Mismatches 0;
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ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 NRIRSNSSAANLMAKKRVIR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 NRIRSNSSAANLMAKKRVIR 313
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LENGTH: 428 amino acids
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                                                                   1 LELYQGIKFEASQKKSAKERKPSTISSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Gaps
                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: WANK, Stephen A.

TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF

TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
82.7%; Pred. No. 4.3e-28;
ive 8; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/AA*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.8%; Score 316; DB 10; Best Local Similarity 82.7%; Pred. No. 4.3e-28; Matches 67; Conservative 8; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASTPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/928,033
PLING DATE: 11-A0C-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/831,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                       308 LNRIRSSSSAANLIAKKKVIR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09443745 Publication No. US20030055238A1
                                                                                                                                                               59 ANRIRSNSSAANLMAKKRVIR
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TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 444 amino acids
amino acid
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Best Local Similarity 82.7
Matches 67; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LELYQCIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kopin, Alan S.
APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR AND USES OF PEPTIDE HORMONE
TITLE OF INVENTION: RECEPTOR AGONISTS
FILE REFERENCE: 00398/118002
CURRENT APPLICATION NUMBER: US/09/401,757
CURRENT PILING DATE: 1998-01-08
PRIOR FILING DATE: 1998-01-08
PRIOR FILING DATE: 1998-12-11
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: No. US20030180798A1 Relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/109002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/428-0200
TELEFAX: 617/438-7045
                                                                                                                                                                                                                              FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/076,510
FILING DATE: 12 MAY 1998
APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.8%; Score 316;
                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq veration 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-127-940-6
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Publication No. US20030191114A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 443 amino acids TYPE: amino acid
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Best Local Similarity 82.7%;
Matches 67; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS
                                                                      COMPUTER READABLE FORM:
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 443
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Query Match

249 LELYQGIKFDASQKKSAKEKKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSR 308

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amino acid
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US-09-864-761-35690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS
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                                                                                                                                  Sequence 23, Application US/09443745
Publication No. US20030055238A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 289.5; DB 10; Length
Pred. No. 4.9e-25;
4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/443,745
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: 08 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/811,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, STEPHEN A.
REGISTRATION NUMBER: 29,768
                    RANRIRSNSSAANLMAKKRVIR 79
  59 ANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 430 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-443-745-23
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                         Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                              RESULT 11
US-09-443-745-23
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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294 RINRIRSSSTANLMAKKRVIR 315

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254 LELYQGIKFDAIQKKSAKERKTSTGSSGPMEDSDGCYLQKSRHPRKLELRQLSPSSSGSN 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>ښ</u>
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Sequence 24, Application US/09443745
Publication No. US20030055238A1
GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIDLE COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/443,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.0%; Score 289.5; DB 10; Best Local Similarity 79.3%; Pred. No. 5.2e-25; Matches 65; Conservative 4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40399/166 NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: 08 029,170
FILING DATE: 10-MAR-1993
APPLICATION NUMBER: US 07/937,609
FILING DATE: 02-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION NUMBER: US 07/811,248
FILING DATE: 07-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 RINRIRSSSSTANLMAKKRVIR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
US-09-443-745-24
US-09-443-745-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 899149
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
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78

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262 ELYRGIQFEMDLNKEAKAHKNGVSTPTTIPSG--DEGDGCYIQVTKRRNTMEMSTLTPSV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ELYQGIKFEASQKKSAKERK----PSTISSGKYEDSDGCYLK-TRPPRKLELRQLSTGS 55
                                                                          1 RKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVI 60
                             KKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVI
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                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10127940
Publication No. US20030180798A1
GENERAL INFORMATION:
APPLICANT: Kopin, Alan S.
APPLICANT: Beinborn, Martin
TITLE OF INVENTION: ASSAY FOR NON-PEPTIDE AGONISTS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: No. US20030180798A1 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.6%; Score 151; DB 14; 42.9%; Pred. No. 6.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 00398/109002 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/076,510
FILING DATE: 12 MAY 1998
APPLICATION NUMBER: 08/570,157
FILING DATE: 11-DEC-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,940
FILING DATE: 23-Apr-2002
CLASSIFICATION: <unreserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 SSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 453 amino acids
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TELEFAX: 617/438-7045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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Best Local Similarity 42.94
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                          RESULT 14
US-10-127-940-7
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A PAPLICANT: How, Wencheng
TITLE OF INVENTION: HUGAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL FOR
TITLE OF INVENTION: HUGAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
TITLE OF INVENTION: HUGAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID
GURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26 6/180,312
PRIOR PELING DATE: 2000-05-26 6/180,312
PRIOR PELING DATE: 2000-05-26 6/180,312
PRIOR PELING DATE: 2000-05-26 6/180,314
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-01-04
PRIOR PELING DATE: 2001-01-05
PRIOR PELING DAT
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Pred. No. 2.2e-25;
0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW271780.1, EVALUE 7.00e-07
P32238, EVALUE 2.00e-75
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ION: EXPRESSED IN BEDAL LIVER, SIGNAL = 2.2

ION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

ON: EXPRESSED IN HERAL, SIGNAL = 2.5

ON: EXPRESSED IN HELAL, SIGNAL = 1.6

N: EXPRESSED IN HELAN, SIGNAL = 1.6

N: EXPRESSED IN HELAN, SIGNAL = 2.1

EXPRESSED IN BT474, SIGNAL = 1.6

EXPRESSED IN BT474, SIGNAL = 1.6

EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

EXTRESSED IN ADULT LIVER, SIGNAL = 1.8

EXTRESSED IN ADULT LIVER, SIGNAL = 1.8

EXPRESSED IN ADULT LIVER, SIGNAL = 1.8

EXTRESSED IN ADULT LIVER, SIGNAL = 1.8

EXTRESSED IN ADULT LIVER, SIGNAL = 1.8

EXTRESSED IN ADULT LIVER, SIGNAL = 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 35690 LENGTH: 176
Sequence 35690, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.8%;
98.4%;
                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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Gaps
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38.6%; Score 151; DB 14; Length 453;
Best Local Similarity 42.9%; Pred. No. 6.3e-09;
Matches 36; Conservative 15; Mismatches 25; Indels 8
Sequence 7, Application US/10441757
GENERAL INFORMATION:
APPLICANT: Kopin, Alan S.
TITLE OF INVENTION: ASAN FOR AND USES OF PEPTIDE HORMONE
TITLE OF INVENTION: RECEPTOR AGONISTS
FILE REFERENCE: 00398/118002
CURRENT APPLICATION NUMBER: US/10/441,757
CURRENT PAPLICATION NUMBER: US/09/004,349
PRIOR PILING DATE: 1998-01-08
PRIOR PILING DATE: 1998-01-08
PRIOR PILING DATE: 1995-12-11
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PSECES OF WINDOWS VERSION 3.0
SEQ ID NO 7
LENGTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-441-757-7
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Search completed:.October 1, 2004, 16:49:06
Job time : 131 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 1, 2004, 16:34:54; Search time 15 Seconds (without alignments) 506.609 Million cell updates/sec Run on:

US-09-841-091B-20 391 Title: Perfect score:

1 LELYQGIKFEASQKKSAKER......NRIRSNSSAANLMAKKRVIR Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database :

summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SGLERATES	
Result No.	Score	Query Match	Query Match Length	DB	•	Description
7	380.5	97.3	428	7	N069	cholecystokinin ty
7	316	80.8	444	~	A42685	cholecystokinin re
m	289.5	74.0	430	7	151898	cholecystokinin A
4	284.5	72.8	436	~	JC5599	cholecystokinin-A
ហ	268	68.5	427	~	850150	gastric CCK-A rece
9	112	28.6	447	N	A47430	gastrin/cholecysto
7	101.5	26.0	450	N	JQ1614	gastrin receptor -
80	98.5	25.2	381	~	S48049	cholecystokinin B
6	. 98.5	25.2	452	~	A46195	cholecystokinin B
10	91.5	23.4	452	7	JC2459	gastrin/cholecysto
11	85.5	21.9	453	7	S32817	gastrin receptor -
12	73	18.7	1359	~	T34036	hypothetical prote
13	71.5	18.3	446	N	A32284	chromogranin A pre
14	71.5	18.3	2823	~	T23064	
15	71.5	18.3	2823	~	F87908	'n
16	71.5	18.3	3102	7	T43291	laminin alpha chai
17	70.5	18.0	533	7	T00742	ubiquitin-binding
18	69	17.6	414	~	A39205	nuclear localizati
	68.5	17.5	580	7	T31529	hypothetical prote
20	67.5	17.3	672	N	H86169	_
21	66.5	17.0	570	-	S50933	
	99	16.9	351	~	T29922	hypothetical prote
	99	16.9	399	Н	OKBYC1	inas
24	99	16.9	537	~	A86444	probable RNA helic
	99	16.9	1641	N	138614	· II
56	65.5	16.8	735	~	S64504	transcription init
	65.5	16.8	1045	7	T18630	hypothetical prote
28	65.5	16.8	7160	7	T27935	
29	65	16.6	470	~	T34402	_

hypothetical prote hypothetical prote	transcription fact	serine/threonine-s	lethal (3) malignant	hypothetical prote	hypothetical prote	hypothetical prote	finger protein XFO	structural protein	hypothetical prote	hypothetical prote	hypothetical prote	NGG1 protein - yea	vitellogenin 1 - m	sperm-specific pro
T00273 T29465	839356	860159	S57844	T29776	T13613	T48079	\$65085	T30349	T18796	T19313	T16917	541685	T43141	865494
~ ~	N	~	~	~	~	7	~	~	7	7	7	7	7	7
1520	644	589	196	1046	1279	1401	232	555	300	333	419	702	1704	101
16.6 16.5	16.5	16.4	16.4	16.4	16.4	16.4	16.2	16.2	16.1	16.1	16.1	16.1	16.1	16.0
65 64.5	64.5	64	64	64	64	64	63.5	63.5	63	63	63	63	63	62.5

ALIGNMENTS

cholecystokinin type A receptor - human

C:Species: Homo sapiens (man) C:Date: 03-Peb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000

C; Accession: JN0692; JN0590 — K; Wank, S.A. R; Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A. Biochen, Biophys. Res. Commun. 194, 811-818, 1993 A; Title: Molecular cloning, functional expression and chromosomal localization of the hun A; Reference number: JN0692; MUID:93343941; PMID:8343165

Accession: JN0692

A; Molecule type: mRNA
A; Residues: 1-428 < DEW>
A; Cross-references (Bs.119315; NID:g306595; PIDN:AAA02819.1; PID:g306596
A; Cross-references (Bs.119315; NID:g306595; PIDN:AAA02819.1; PID:g306596
A; Experimental source: gallbladder
R; Ulrich, C.D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.; Miller, L.J.
Biochem: Biophys. Res. Commun. 193, 204-211, 1993
A; Title: Molecular cloning and functional expression of the human gallbladder cholecysto)
A; Reference number: JN0590; MUID:93277552; PMID:8503909
A; Status: nucleic acid sequence not shown
A; Molecule type: DNA

A; Residues: 1-428 <ULR>

A;Cross-references: GB:L13605; NID:g306490; PIDN:AAA35659.1; PID:g306491
A;Experimental source: gallbladder
C;Comment: This protein has diverse physiological roles in the gastrointestinal system which, and secretion from gastric mucosal cells.

C;Genetics:
A;Gene: GDB:CCKAR
A;Gene: GDB:141927; OMIM:118444
A;Map position: 4pter-4qter

Gisuperfamily: neurokinin receptor
Gisuperfamily: neurokinin receptor
Gisuperfamily: neurokinin receptor; glycoprotein; hormone receptor; phosphoprotein; t
F;40-67/Domain: transmembrane #status predicted <TM1>
F;78-104/Domain: transmembrane #status predicted <TM2>
F;78-104/Domain: transmembrane #status predicted <TM3>
F;158-17/Domain: transmembrane #status predicted <TM3>
F;158-134/Domain: transmembrane #status predicted <TM5>
F;30-34/Domain: transmembrane #status predicted <TM5>
F;310-34/Domain: transmembrane #status predicted <TM5>
F;350-369/Domain: transmembrane #status predicted <TM7>
F;10,24,190,299/Binding site: carbohydrate (Ser) (covalent) (by protein kinase C) #status F;256/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status F;256/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Gaps 1; DB 2; Length 428; Indels 97.3%; Score 380.5; DB 2; 98.8%; Pred. No. 6.9e-33; iive 0; Mismatches 0; Query Match Best Local Similarity 98.8 Matches 79; Conservative

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Gaps

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10; Indels

Length 430;

293

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R,De Weerth, A.; Pisegna, J.R.; Wank, S.A.
Am. J. Physiol. 265, Gll16-Gll21, 1993
A,Fille: Gulinea pig gallbladder and pancreas possess identical CCK-A receptor subtypes: 1
A,Fille: Gulinea pig gallbladder and pancreas possess identical SCK-A receptor subtypes: 1
A,Reference number: I51898
A,Recession: I51898
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholecystokinin-A receptor - mouse
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house cervision 23-Sep-1997 #text_change 20-Apr-2000
Rilacourse, K.A.; Lay, J.M.; Swanberg, L.J.; Jenkins, C.; Samuelson, L.C.
Biochem: Biophys. Res. Commun. 236, 630-635, 1997
A;Tile: Molecular structure of the mouse CCK-A receptor gene.
A;Reference number: JCS599; MUID:97396148; PMID:9245702
A;Reference number: JCS599; MUID:97396148; PMID:9245702
A;Reference number: JCS599; MUID:97396148; PMID:9245702
A;Reference number: JCS599
A;Reference 
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Dates: 14-U1-1995 #sequence_revision 21-Ju1-1995 #text_change 20-Apr-2000
C;Accesion: S50150
R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.
A;Reference number: S50150; MUID:95002144; PMID:7918628
A;Accession: S50150
A;Accession: S50150
A;Restdues: 1-427 <REU>
C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LELYQGIKFEASQKKSAKERKPST-----TSSGKYEDSDGCYL-KTRPPRKLELRQLS
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-430 <RES.
A; Cross-references: GB:S68242; NID:g544723; PIDN:AAB29504.1; PID:g544724
C; Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.8%; Score 284.5; DB 2; 71.6%; Pred. No. 1.1e-22;
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Pred. No. 3.3e-23;
4; Mismatches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 TGSS-SRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 RINRIRSSSSTANLMAKKRVIR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65; Conservative
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Best Local Similarity
Matches 65; Conserv
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Best Local S
Matches 63
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A,Statuus: preliminary
A,Molecule type: protein
A,Residues: 166-189 <MAN>
C,Comment: This G-protein-coupled receptor is present in the gastrointestinal system, va
smooth muscle contraction of the gallbladder and stomach. It is capable of activating
ducing the subsequent release of intracellular calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of the cholecystokin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Mantamadiotis, T.; Baldwin, G.S.
Blochem. Biophys. Res. Commun. 201, 1382-1389, 1994
A;Title: The seventh transmembrane domain of gastrin/CCK receptors contributes to non-pe
A;Reference number: PC2213; MUID:94296413; PMID:8024583
                                                                                                                                                                                                                                                               Ad2685

cholecystokinin receptor type A - rat

cholecystokinin receptor type B - rat

cholecystokinin receptor type B - rat

cholecystokinin Receptor revision Relocation Receptor R
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C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
F;57-82/Domain: transmembrane #status predicted aTM1.
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C;Species: Cavia porcellus (guinea pig)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Apr-2000
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                                                                                      294 NRIRSNSSAANLMAKKRVIR 313
NRIRSNSSAANLMAKKRVIR 79
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<u>ب</u>

Gaps

6

6; Indels

Length 436;

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C;Accession: JQ1614
R;Nakata, H.; Matsui, T.; Ito, M.; Taniguchi, T.; Naribayashi, Y.; Arima, N.; Nakamura, P
Biochem. Biophys. Res. Commun. 187, 1151-1157, 1992
A;Title: Cloning and characterization of gastrin receptor from ECL carcinoid tumor of Mas A;Reference number: JQ1614; MUID:92412082; PMID:1530611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: J01614
A; Molecule type: MRNA
A; Residues: 1-450 «NAKA
A; Residues: 1-450 «NAKAA
A; Residues: 1-450 «NAK
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C;Date: 07-May-1995 #sequence_revision 01-Nov-1996 #text_change 20-Apr-2000
C;Date: 07-May-1995 #sequence_revision 01-Nov-1996 #text_change 20-Apr-2000
C;Accession: 548049
N. Neurochem. 63, 1199-1206, 1994
A;Title: 1dentification and characterization of various cholecystokinin B receptor mRNA A;Reference number: 848049, MUID:95016646; PMID:7931273
A;Accession: 848049
A;Accession: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-381 cJAGS
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F;7.30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;7.30,154,300,442/Binding site: phosphate (Ser) (covalent) #status predicted
F;81.27-205/Disulfide bonds: #status predicted
F;321/Binding site: phosphate (Thr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gāstrin receptor - multimammate rat (Mastomys natalensis)
C;Species: Mastomys natalensis
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ELYQGIKFEASQKKSAKER----KTR----KPSTTSSGKYEDSDGCYL---KTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EDSDGCYLKTRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Gaps
                                                                                                                                                                                                                                                                                                                                                          ; DB 2; Length 447; 0.00026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 P--ALELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 PPRKLELRQLST---GSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|:| |:||:||:| 336
F;334-354/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101.5; DB 2;
Pred, No. 0.0035;
8; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ELYQGIKFEASQKKSAKER-----KPSTTSSGKY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          28.6%; Score 112; 33.7%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 33.78
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Conservative
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo saplens (man)
C;Date: 25-Feb-1994 #sequence revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A47430; JC1352; A46645; A48262
R;Ito, M; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.; Nakata, H.
S;Ito, M; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.; Nakata, H.
J; Biol. Chem. 268; 18300-18305, 1993
A;Title: Functional characterization of a human brain cholecystokinin-B receptor. A trop A;Reference number: A47430
A;Reference number: A47430
A;Residues: 1-47 (MD:)
A;Residues: 1-47 (ATO)
A;Residues: 1-47 (ATO
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C,Superfamily: neurokinin 1 receptor
C,Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone rece
F;57-81/Domain: transmembrane #status predicted <TM1>
F;91-116/Domain: transmembrane #status predicted <TM3>
F;131-150/Domain: transmembrane #status predicted <TM3>
F;171-192/Domain: transmembrane #status predicted <TM3>
F;171-192/Domain: transmembrane #status predicted <TM3>
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R; Lee, Y.M.; Beinborn, M.; McBride, E.W.; Lu, M.; Kolakowski Jr., L.F.; Kopin, A.S.
J. Biol. Chem. 268, 8164-8169, 1993
A; Title: The human brain cholecystokinin-B/gastrin receptor. Cloning and characterizatic
A; Reference number: A46645; MUID:93216795; PMID:7681836
A; Accession: A46645
A; Status: nucleic acid sequence not shown; not compared with conceptual translation
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R;Song, I.; Brown, D.R.; Wiltshire, R.N.; Gantz, I.; Trent, J.M.; Yamada, T.
Rpcc. Natl. Acad. Sci. US.A. 90, 9085-9089, 1999
A;Title: The human gastrin/cholecystokinin type B receptor gene: alternative splice donc A;Reference number: A48262; MUID:94022320; PMID:8415658
                                                                                                                                                                                                                                                                                                                    RESULT 6
447430
gastin/cholecystokinin receptor B, short splice form - human
N,Alternate names: CCK-B/gastrin receptor; cholecystokinin-B/gastrin receptor
                                                                                                                                                                                                                                                         1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGSSSRA 59
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A,Residues: 1-447 <PIS>
A,Cross-references: GB:L04473; NID:g179997; PIDN:AAA35660.1; PID:g179998
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A;Residues: 1-447 <RES>
A;Cross-references: GB:L10822; NID:g406075; PIDN:AAC37528.1; PID:g406076
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A;Residues: 1-447 <LEE>
A;Cross-references: GB:L08112; NID:g306488; PIDN:AAA35657.1; PID:g306489
                                                                                                                                                       5
                                                Length 427;
                                                                                                                                                       10; Indels
                                                Score 268; DB 2;
Pred. No. 6.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                           68.5%; Score 71.2%; Pred. No. 6.4e.
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A;Introns: 51/1; 135/1; 218/2; 271/1
                                           Query Match
Best Local Similarity 71.2%
Matches 57; Conservative
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42

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Gaps

31;

-----KPSTTSSGKYEDSDGCYL-

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242 ELYLGLRFDSDSBSESQSRVRGQGGLPGGAAPGPVHQNGRCRPEAGLAG--EDGDGCYVQ 299
                                                                                                                        23.4%; Score 91.5; DB 2; Length 452; 29.1%; Pred. No. 0.04; tive 15; Mismatches 27; Indels 3:
                                                                                                                                                                                                                                                                                                                                                            39 -- KTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR
         F;217-237/Domain: transmembrane #status predicted <TM5>F;339-359/Domain: transmembrane #status predicted <TM6>F;381-400/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                          2 ELYQGIKFEASQKKSAKER-----
                                                                                                                                                                                    Conservative
                                                                                                                                             Local Similarity
nes 30; Conserv
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                                                                                                                        Query Match
Best Local S:
Matches 30
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Best Local Si
Matches 28;
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Peb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Apr-2000
C;Accession: JC2459
R;Blandizzi, C.; Song, I.; Yamada, T.
Biochem. Biochem. Biochem. Sepubys. Res. Commun. 202, 947-953, 1994
A;Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptor A;Reference number: JC2459; MUID:94324990; PMID:8048969
A;Accession: JC2459; MUID:94324990; PMID:8048969
A;Accession: JC2459; MUID:94324990; PMID:8048969
A;Residues: 1-452 - BLA>
A;Cross-references: GB:L31548; NID:g495663; PIDN:AA31194.1; PID:g495665
C;Genetics:
A;Introns: 49/1; 133/1; 216/2; 273/1
C;Superfamily: neurokinin | receptor
C;Superfamily: neurokinin | receptor
C;Superfamily: neurokinin | receptor
C;Superfamily: transmembrane #status predicted <TM1>
F;85-79/Domain: transmembrane #status predicted <TM1>
F;130-149/Domain: transmembrane #status predicted <TM3>
F;169-187/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A46195

A46195

Cholecystokinin B receptor subtype - rat

C;Species: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000

C;Accession: A46195

Ryank, S.A.; Pisegna, J.R.; de Weerth, A.

Proc. Natl. Acad Sci. U.S.A. 89, 8691-8695, 1992

A;Title: Brain and gastrointestinal cholecystokinin receptor family: structure and funct
A;Reference number: A46195; MUID:92409582; PMID:1528881
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994 C;Genetics: 64/2; 147/2; 205/1
C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                2 BLYQGIKFEASQKKSAKER-------KPSTTSSGKYEDSDGCYLK 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Note: sequence extracted from NCBI backbone (NCBIN:114083, NCBIP:114084)
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.2%; Score 98.5; DB 2; Length 452;
30.0%; Pred. No. 0.0073;
tive 14; Mismatches 29; Indels 27; Gaps
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-452 <WAN>
A/Cross-references: GB.M99418; NID:g203459; PIDN:AAA40925.1; PID:g203460
                                                                                                                                                                                                            27;
                                                                                                                                                   Length 381;
                                                                                                                        25.2%; Score 98.5; DB 2; Lengui JU. 30.0%; Pred. No. 0.0061;
                                                                                                                                                                                                                                                                                                                                                                                                                     231 L-PRSRLEMITLITPIPGPVPGPRPNQ--AKLLAKKRVVR 267
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                                                                                                                                                                                                                                                                                                                                                                              40 TRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR 79
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                                                                                                                                                                                                         30; Conservative 14; Mismatches
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Best Local Similarity 30.09
Matches 30, Conservative
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                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                   Query Match
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Gastrin receptor - dog

Gispecies: Canis lupus familiaris (dog)
Cispecies: Canis lupus familiaris
Rikopin, A.S.; Lee, Y.M.; McBride, E.W.; Miller, L.J.; Lu, M.; Lin, H.Y.; Kolakowski Jr., Proc. Natl. Acas. Sci. U.S.A. 89, 3605, 1992
A.Tile: Expression cloning and characterization of the canine parietal cell gastrin recentation: S22817
A.Feference number: S32817
A.Feference number: S32817
A.Feference numbay
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-453 <KOP>
A.Cross-references: EMBL.M87834; NID:g163956; PIDN:AAA30847.1; PID:g163957
C; Superfamily: neurokinin 1 receptor
C; Superfamily: neurokinin 1 receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Accession: T34036
A; Pulton, R.; Wohldmann, P.
Submitted to the EMBL Data Library, April 1997
A; Description: The sequence of C. elegans cosmid B0041.
A; Reference number: Z21466
A; Accession: T34036
A; Accession: T34036
A; Actus: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1359
A; Residues: 1-1359
A; Cass-references: EMBL: AF000196; PIDN: AAC24256.1; GSPDB: GN00019; CESP: B0041.7
A; Experimental source: strain Bristol N2; clone B0041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 21.9%; Score 85.5; DB 2; Length 453; 1 Similarity 28.3%; Pred. No. 0.18; 28; Conservative 14; Mismatches 32; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 18.7%; Score 73; DB 2; Length 1359; Best Local Similarity 31.5%; Pred. No. 11; Matches 23; Conservative 12; Mismatches 34; Indels
300 LPRSRP--ALELSALTAPISGPGPR--PAOAKLLAKKRVVR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 ŔSRQTĽEĽSAĽTAPTPGPGGGPRPYQ--ÁKĽLÁKKRVVR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 RPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR
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Indels 15;

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A;Map position: 1
A;Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology skeference number: A;Sto() MID199069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 1
C,Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like ho
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;Residues: 1-2823 <STO>
;Cross-references: GB:chr_1; PIDN:CAA15432.1; PID:g3924779; GSPDB:GN00019; CESP:T22A3.8
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A;Residues: 1-2823 <ST2>
A;Cross-references: GB:chr_1; PIDN:CAB0338S.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.
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A;Residues: 1-2023 «MI2>
A;Cross-references: EMBL:281125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
A;Experimental source: clone T22A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 QGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYLKTRPPR-----KL-ELRQLSTGS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein T22A3.8 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-Aug-2001
C;Accession: F87908 E87908
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 18.3%; Score 71.5; DB 2; Length 2823; Best Local Similarity 34.2%; Pred. No. 34; Matches 27; Conservative 13; Mismatches 24; Indels 15;
       preliminary; translated from GB/EMBL/DDBJ
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18.3%; Score 71.5; DB
Best Local Similarity 34.2%; Pred. No. 34;
Matches 27; Conservative 13; Mismatches
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Job time: 17 secs
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A; Status: preliminary
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A,Gene: CESP:T22A3.8
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A;Title: Pancreastatin, a novel pancreatic peptide that inhibits insulin secretion.
A;Reference number: A26419; MUID:87065127; PMID:3537810
A;Molecule type: protein
A;Residues: 256-304 cIAT>
C;Reywords: amidated carboxyl end; calcium binding; carbohydrate metabolism; glycoprotei
E;256-304/Product: pancreastatin #status experimental cPCN>
E;304/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                        A32284

Assistant A precursor - pig (fragment)

NyAlternate names: secretory protein;
NyAlternate names: secretory protein;
NyAlternate names: secretory protein;
NyContains: beta-granin; chromostatin; pancreastatin; parastatin; vasostatin
C;Species: Sus acrofa domestica (domestic pig)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 16-Jul-1999
C;Accession: A32284; A26419
R;Iacangelo, A.L.; Fischer-Colbrie, R.; Koller, K.J.; Brownstein, M.J.; Eiden, L.E.
Bandocrinology 122, 23139-2341, 1988
A;Title: The sequence of porcine chromogranin A messenger RNA demonstrates chromogranin
A;Reference number: A32284; MUID:88196011; PMID:2834189
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A;Cross-references: EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8
                                             || :| : || || ::|::| | : || || ELKEGTE-EASSKEAAEKRGDSKEVEKNDEDAGAKPQASLEPPXXXEAEDQTPGEEEAA 172
8 KFEASQKKSAKERKPSTISSGKYEDSD-GCYLKTRPPRKLELRQLSTGSSSRA---NRIR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #abdroc_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T23064; T25096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, October 1996
A;Reference number: Z19980
A;Accession: T25096
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                                                                                                                                                                                                                  167 KSKKNKEKSVKKR 179
                                                                                                                                                 64 SNSSAANLMAKKR 76
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A; Molecule type: mRNA
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DB 2; Length 2823; Indels

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

October 1, 2004, 16:33:33; Search time 9 Seconds (without alignments) 457.060 Million cell updates/sec

US-09-841-091B-20 391 1 LELYQGIKFEASQKKSAKER.....NRIRSNSSAANLMAKKRVIR 79 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		_			097772 oryctolagus		P32239 homo sapien		-		P79266 bos taurus	-	P30552 canis famil	Q9u7e0 caenorhabdi	P04404 sus scrofa	P27476 Baccharomyc	Q9z0e3 mus musculu	sacch		pan t					_		_	_		P32494 saccharomyc	Q90508 fundulus he	Q44342 agrobacteri	7k1
SUMMARIES		CCKR_RAT		CCKR_MOUSE	CCKR_RABIT	CCKR_XENLA	GASR HUMAN	GASR_MOUSE	GASR_PRANA	GASR_RAT	GASR_BOVIN	GASR_RABIT			CMGA_PIG	NSR1_YEAST	AIRE_MOUSE	KAPA_YEAST	ATRX_HUMAN	ATRX_PANTR	ATRX_PONPY	T2FA_YEAST	CZF1_CANAL	BTD_DROME	MBN DROME	Y232 HUMAN		RRSI_CAEEL	STE7_CANAL	ADA3_YEAST	VIT1 FUNHE	FLGH AGRT5	IF2_LEPIN
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PHI1_MYTED T2FA_HUMAN	DD20_HUMAN T150_HUMAN VIT1_CHICK	SFRC_MOUSE FXH1_XENLA KAPC_YEAST	PLAK_HUMAN T3RE_SALTY ROAA_MOUSE	ROAA_HUMAN
п п				Н
91	824 955 1912	494 518 398	743 990 285	331
15.7	15.6 15.6 15.6	15.5 15.5 15.3	15.3 15.3 15.2	15.2
61.5 61.5	61 61	60.5 60.5 60	60 60 59.5	59.5
34 35	36 37 38	39 4 4 0 11 0	4 4 4 0 6 4	45

ALIGNMENTS

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CARBOHYD
DISULFID
LIPID
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                      RESULT 2
                               CCKR_RAT
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R EMBL; U23429; AAA91123.1; ---
R EMBL; U23429; AAA91123.1; JOINED.
R EMBL; U23429; AAA91123.1; JOINED.
R EMBL; U23429; AAA91123.1; JOINED.
R EMBL; U23429; AAP84362.1; ---
R EMBL; D85606; BAA90879.1; ---
R EMBL; DN692; JN0692.
R PDB; 1D6G; 17-N0V-99.
R PDB; 1D6G; 17-N0V-99.
R PDB; 1B7, 25-APR-01.
R Genew; HGNC:1570; CCKAR.
R MIM; 118444; ---
GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0005887; C:integral to plasma membrane; TAS.
R GO; GO:0007504; P:cytosolic calcium ion concentration elevation; TAS.
R GO; GO:0007584; P:response to nutrients; TAS.
R GO; GO:0007584; P:response to nutrients; TAS.
R FAM; PRO0001; 7tm 1; 1.
R PRINTS; PRO001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LELYOGIKFEASOKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELROLSTGSSSRA
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N.LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
S-palmitoyl cysteine (By similarity).
AGEBFABDA805E610 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 380.5; DB 1; Length 428; Pred. No. 2.6e-33; 0; Mismatches 0; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
(YTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47841 MW;
                                                                                                                                          EMBL; L13605; AAA35659.1; -. EMBL; L19315; AAA02819.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.3%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.c.
79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           428 AA;
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                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                         Purification, molecular cloning, and functional expression of the cholecystokinin receptor from rat pancreas.";

Proc. Natl. Acad. Sci. U.S.A. 89:3125-3128(1992).

-!- FUNCTION: Receptor for cholecystokinin. Has a 1000 fold affinity for CCK rather than for gastrin. It modulates feeding and dopamine-induced behavior in the central and peripheral nervous system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: Pancreas and brain.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 111-158; 270-314 AND 392-402
                                                                                                                                                                                                                                                                                                                TIŜSUE=Pancreas;
MEDLINE=92212981; PubMed=1313582;
Wank S.A., Harkins R., Jensen R.T., Shapira H., de Weerth A.,
Slattery T.;
                                           01-APR-1993 (Rel. 25, Created)
1-APR-1993 (Rel. 25, Last sequence update)
10-0CT-2003 (Rel. 42, Last amotation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A42685; A42685.
HSSP; P02699; IF88.
Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODDESN.
PROSITE; PS00237; G_PCRRHODDEN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
G-protein, coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
444 AA.
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STANDARD;
                                                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein, Palmitate
                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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DOMAIN
  CCKR RAT
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S-palmitoyl cysteine (By similarity).

'n

3; Gaps

Score 289.5; DB 1; Length 430; Pred. No. 1.3e-23; 4; Mismatches 10; Indels 3

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINED (GLCNAC. .) (POTENTIAL).

CYTOPLASMIC (POTENTIAL)

6 (POTENTIAL)

S-palmitoyl cysteine (By similarity) FC9F5D34032076C9 CRC64;

48210 MW; 74.0%; 79.3%;

BY SIMILARITY

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1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS--SS 57
                                                                                                                                                                                                                                                                                                                                                                    58 RANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF015963; AAC07949.1; -.
                                                                                                                                                                                                                         Query Match
Best Local Similarity 79.3
Matches 65; Conservative
                                                                                                                                                                          389 3
430 AA;
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CARBOHYD
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DISULFID
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                                                                                                       CARBOHYD
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DOMAIN
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                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Gall bladder, and Pancreas;

X MEDLINE-94106629; PubMed-7916580;
A de Weerth A., Pisegna J. R., Wank S.A.;
de Weerth A., Pisegna J. R., Wank S.A.;
T "Guinea pig gallbladder and pancreas possess identical CCK-A receptor "T "Guinea pig gallbladder and pancreas possess in the complex to the complex to
                                                                                                                       1 LELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGCYL-KTRPPRKLELRQLSTGS-SSR
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                    ,
,
                                    Length 444;
                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoctation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR00276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS502627; G PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
444 AA; 49657 MW; B435BE7505C2FB11 CRC64;
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EXTRACELLULAR (POTENTIAL)
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                                  Score 316; DB 1;
Pred. No. 2.1e-26;
                                                                                                                                                                                                                                                                                                430 AA.
                                                                    8; Mismatches
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                                                                                                                                                                                            309 LNRIRSSSSAANLIAKKRVIR 329
                                                                                                                                                                        59 ANRIRSNSSAANLMAKKRVIR 79
                                  80.8%;
82.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S68242; AAB29504.1; -.
                                                                    Conservative
                                                                                                                                                                                                                                                                                                STANDARD;
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DOMAIN 1 41
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HSSP; P02699; 1F88.
                           Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lacourse K.A., Lay J.M., Swanberg L.J., Jenkins C., Samuelson L.C.;
"Molecular structure of the mouse CCK-A receptor gene.";
Biochem. Biophys. Res. Commun. 236:630-615(1997).

-i- FUNCTION: Receptor for cholecystokinin. Has a 1000 fold affinity for CCK rather than for gastrin. It modulates feeding and dopamine-induced behavior. In the central and peripheral nervous system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               messenger system.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takata Y., Takiguchi S., Takaoka K., Funakoshi A., Miyasaka K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholecystokinin type-A receptor gene and its structural
                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
0-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR).
294 RINRIRSSSSTANLMAKKRVIR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SvJ; TISSUE=Liver;
MEDLINE=97254481; PubMed=9099891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvJ;
MEDLINE=97396148; PubMed=9245702;
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 187:267-271(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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P70031;
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DOMAIN
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DISULFID
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TRANSMEM
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DOMAIN
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CCKR_XENLA
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Reuben M., Rising L., Prinz C., Hereey S., Sachs G.;
"Cloning and expression of the rabbit gastric CCK-A receptor.";
Biochim. Biophys. Acta 1219:321-327(1994).
-i- FUNCTION: Receptor for cholecystokinin. Has a 1000 fold affinity
for CCK rather than for gastrin. It modulates feeding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cholecystokinin type A receptor (CCK-A receptor) (CCK-AR)
                                                                                                                     MGD; MGI:99478; Cckar.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROSITE; PR00037; GFCRHODOPSN.
PROSITE; PS00237; GFROTEIN RECEP F1 1; 1.
PROSITE; PS00267; GFROTEIN, RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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YTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Conservative 10; Mismatches
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EMBL; AF015959; AAC07949.1; JOINED. EMBL; AF015960; AAC07949.1; JOINED. EMBL; AF015961; AAC07949.1; JOINED. EMBL; AF015962; AAC07949.1; JOINED. EMBL; BS605; BAA20068.1; -. PIR; JCS599; JCS599.
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436 AA;
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nes 63; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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dopamine-induced behavior in the central and peripheral nervous system. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system (By similarity).

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLONAC. . ) (POTENTIAL).
N-LINKED (GLONAC. . ) (POTENTIAL).
N-LINKED (GLONAC. . ) (POTENTIAL).
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-stokinin receptor (CCK-XLR).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-palmitoyl cysteine (By similarity) 089FD10E2B86DB25 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interprof. IPR000276, GPCR_Rhodpsn.
Pfam; PF00001, 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS00262; G_PROTEIN RECEP F1 2; 1.
G-protein Coupled receptor; Transmembrane; Glycoprotein;
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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HSSP; P02699; 1F88.
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Matches 58; Conservative
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447 AA.

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01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pisegna J.R., de Wearth A., Huppi K., Wank S.A.; "Molecular cloning of the human brain and gastric cholecystokinin receptor: structure, functional expression and chromosomal
                                                                                                                                                                                                                                    Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          MEDLINE-93216795; PubMed=7681836;
Lee Y.-M., Beinborn M., McBride B.W., Lu M., Kolakowski L.F. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                        Kopin A.S.; "The human brain cholecystokinin-B/gastrin receptor. Cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ochem. Biophys. Res. Commun. 189:296-303(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 268:8164-8169(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93080572; PubMed=1280419;
                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                          CCKBR OR CCKRB
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                                                             HUMAN
                                           GASR_HUMAN
                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                "Identification of cholecystokinin-B/gastrin receptor domains that confer high gastrin affinity: utilization of a novel Xenopus laevis cholecystokinin receptor.";
Mol. Pharmacol. 50:436-441(1996).
-I- FUNCTION: Receptor for cholecystokinin. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system. Has high affinity for CCK-8 and low affinities for gastrin-17-I, CCK-4, and unsulfated CCK-8.
                                       MEDLINE=96319796; PubMed=8700154;
Schmitz F., Pratt D.S., Wu M.-J., Kolakowski L.F. Jr., Beinborn M.,
                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Brain and stomach.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
HAS EQUAL SIMILARITY TO TYPE A AND B CHOLECYSTOKININ MAMMALIAN
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8.3e-09;
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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BY SIMILARITY.
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453 AA;
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&$\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{
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-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ż
                                                                                                                                                          "The human gastrin/cholecystokinin type B receptor gene: alternative splice donor site in exon 4 generates two variant mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 90:9085-9089(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kopatz S.A., Aronstam R.S., Sharma S.V.;

"CDRA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity. This receptor mediates its action by association with G proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ito M., Matsui T., Taniguchi T., Tsukamoto T., Murayama T., Arima Nakata H., Chiba T., Chihara K.; Fuctional characterization of a human brain cholecystokinin-B receptor. A trophic effect of cholecystokinin and gastrin."; J. Biol. Chem. 268:18300-18305(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tate S.N., Gray J., Denyer J., Stolz M., Foord S., Lee M.G.; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
TISSUE=Placenta;

BEDLINE=94022320; PubMed=8415658;
Song I., Brown D.R., Wiltshire R.N., Gantz I., Trent J.M., Yamada T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93352657; PubMed=8349705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Temporal cortex;
Tate S.N., Gray J., Den;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        rissum=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rissum=Brain;
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ELYQGIKFEASQKKSAKERK----PSTTSSGKYEDSDGCYLK-TRPPRKLELRQLSTGS 55

79

SSRANRIRSNSSAANLMAKKRVIR

26

8

320 CTKMDRARINNSEAKLMAKKRVIR 343

Gaps

8;

25; Indels

; Pred. No. 8.36

42.9%;

Local Similarity 42.9 tes 36; Conservative

Matches

N

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GASR
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R GO, 60008881; C:integral to plasma membrane; TAS.

R GO, 60008881; E:cholecystckinin receptor activity; TAS.

R GO, GO:0004591; F:cholecystckinin receptor activity; TAS.

R GO; GO:0004591; F:cholecystckinin receptor activity; TAS.

R GO; GO:0007203; F:chosphatidylinositol 3-kinase regulator act. .; TAS.

R GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.

R GO; GO:0007204; P:cell surface receptor linked signal transdu. .; TAS.

R GO; GO:0007204; P:cell surface receptor linked signal transdu. .; TAS.

R GO; GO:0007203; P:phosphatidylinositol.4,5-bisphosphate hydro. .; TAS.

R GO; GO:0007503; P:sensory perception; TAS.

R InterPro; IPR00276; GPCR_Rhodpsn.

R RNINTS; PR000217; GPCRRHODPSN.

R PROSITE; PS50227; GPRRHODPSN.

R PROSITE; PS50226; G PROTEIN RECEP_F1_1; 1.

R PROSITE; PS50226; G PROTEIN RECEP_F1_2; 1.

R PROSITE; PS50226; G PROTEIN RECEP_F1_2; 1.

R PROMICATE: PS100277; GPCRHODPSN.

R PROMICATE: PS
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S-palmitoyl cysteine (By similarity).

L -> F (in dabsNP:1805000).

/FTIG=VAR. 014664.

V -> I (in dabsNP:1805002).

/FTIG=VAR. 014685.

R -> H (in dasNP:1805004).

/FTIG=VAR. 014686.

R -> Q (in dasNP:1805001).

/FTIG=VAR. 014686.

L -> Q (in dasNP:1805001).

/FTIG=VAR. 014687.

A -> P (IN REF. 5).

L -> V (IN REF. 5).

MW, BABEEFAD4CIF85915 CRC64;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUTAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR.
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                   EMBL; L08112; AAA35657.1; --
EMBL; L04473; AAA35660.1; --
EMBL; L10822; AAC37528.1; --
EMBL; D13305; BAA02564.1; --
EMBL; L07746; AAA91831.1; --
EMBL; AY32551; AAP84364.1; --
EMBL; AY32551; AAP84364.1; --
PDB; L147; 28.7AN-03.
Genew; HONC:1571; CCKBR.
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447 AA;
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41

---KPSTTSSGKYEDSDGCYL---KTR

ELYQGIKFEASQKKSAKER--

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244 ELYLGLRFDGDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVG--EDSDGCYVQLPRSR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blochem. Biophys. Res. Commun. 272:837-842(2000).

-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system (By similarity).
-!- SUBCELJULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=129/SvJ;
MEDLINE=20318371; PubMed=10860839;
Lay J.M., Jenkins C., Friis-Hansen L., Samuelson L.C.;
"Structure and developmental expression of the mouse CCK-B receptor
                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:99479; Cckbr.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS50262; GPROTEIN RECEP F1 1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                 Kopin A.S.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                    302 P--ALELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
                                42 PPRKLELROLST---GSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                  453 AA
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EMBL; AF264178; AAG09801.1; -.
EMBL; AF264177; AAG09801.1; JOINED.
                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein; Palmitate
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                 GASR MOUSE
P56481;
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                                                                                                                                   MOUSE
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                                                                                                                                                                                                                                                           244 ELYLGIRFDGDNDSETQSRVRNQGGLPGGAAAPGPVHQNGGCRHVTSLIG--EDSDGCYV 301
                                                                                                                                                                                                                                        -----KPSTTSSGKYEDSDGCYL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92412082; PubMed=1530611;
Nakata H., Matsui T., Ito M., Taniguchi T., Naribayashi Y., Arima N.,
Nakamura A., Kinoshita Y., Chihara K., Hosda S., Chiba T.;
Nakamura A., Kinoshita Y., Chihara K., Hosda S., Chiba T.;
"Cloning and characterization of gastrin receptor from ECL carcinoid
tumor of Matcomys natalensis.";
Biochem. Biophys. Res. Commun. 187:1151-1157(1992).
-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B
receptors occur throughout the central nervous system where they
modulate anxiety, analgesia, arousal, and neuroleptic activity.
This receptor mediates its action by association with G proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Stomach and brain. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Praomys natalensis (African soft-furred rat) (Mastomys natalensis)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that activate a phosphatidylinositol-calcium second messenger
             CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BY SIMILARITY.
                                                                                                          S-palmitoyl cysteine (By similarity) DFD21432C323405C CRC64;
                                                                                                                                                                                                    28;
                                                                                                                                                              Length 453;
                                                                                                                                                                  PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                    : | :||:||:||:| OL-PRSRLEMTTLTTPTTGPGPGPRPNQ--AKLLAKKRVVR 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                               39 KTRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            450 AA
 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (POTENTIAL)
                                                                                                                                                                Score 103;
                                                                                                                                                                                                                                        2 ELYQGIKFEASQKKSAKER------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                    16;
                                                                                                                             49171 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D12817; BAA02250.1; -.
                                                                                                                                                                26.3%;
                                                                                                                                                                                 29.78;
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein, Palmitate.
DOMAIN 1 57
                                                                                                          414
453 AA;
                                                                                                                                                                                   Local Similarity
tes 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mastomys.
NCBI_TaxID=10112;
                                                                                                                                                                                                                                                                                                                                                                                                                                            GASR PRANA
                                                                    CARBOHYD
DISULFID
                                                                                                          LIPID
SEQUENCE
TRANSMEM
DOMAIN
                                      CARBOHYD
                                                     CARBOHYD
                                                                                                                                                              Query Match
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GASR_PRANA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsetion-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                     -----EDSDGCYLKTRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wank S.A., Pisegna J.R., de Weerth A.;
"Brain and gastrointestinal cholecystokinin receptor family:
structure and functional expression.";
Proc. Natl. Acad. Sci. U.S.A. 89.861-8695(1992).
-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B
receptors occur throughout the central nervous system where they
modulate anxiety, analgesia, arousal, and neuroleptic activity.
This receptor mediates its action by association with G proteins
that activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein. TISSUE SPECIFICITY: Parietal cells, pancreas, brain and various
                                                                                                                                6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neoplastic tissues.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
10-APR-1993 (Rel. 25, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoutation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                           S-palmitoyl cysteine (By similarity)
EF13BA8B5FAA857A CRC64;
                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                          DB 1; Length 450;
                                                                                                                                                                                                                                                                                                                                        Indels
                2 (POTENTIAL).
EXTRACELULAR (POTENTIAL)
                                                                        4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                           3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                        5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336
                                                                                                                                                                                                                                                                                                                                                                     2 ELYQGIKFEASQKKSAKER-----KPSTISSGKY----
                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                  43 PRKLELROLSTGSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 RSRLEMTTLTTPTPGPG---LASANQAKLLAKKRVVR
                                                                                                                                                                                                                                                                                                          26.0%; Score 101.5; DB 28.9%; Pred. No. 0.0016;
                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 AA
                                                                                                                                                                                                                                                                                                                                        18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain; MEDLINE=92409582; PubMed=1528881; MEDLINE=92409582; PubMed=1528881;
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Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
87
1131
1131
1130
1140
1189
1189
1242
1346
1358
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1358
                                                                                                                                                                                                                                                              411
450 AA;
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DOMAIN
TRANSMEM
DOMAIN
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TRANSMEM
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GASR_RAT
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EMBL; S83090; AAB46896.1; -.
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454 AA;
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P46627;
                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
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TRANSMEM
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RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 ELYLGLHFDGENDSETQSRARNQGGLPGGAAPGPVHQNGGCRPVTSVAG--EDSDGCCVQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                             -----KPSTISSGKYEDSDGCYLK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Pancreas;

MEDLINE-97003669; PubMed-8851180;

MEDLINE-97003669; PubMed-8851180;

MEDLINE-97003669; PubMed-8851180;

MEDLINE-97003669; PubMed C., Clerc P., le Huerou-Luron I., Frats H.,

Bertrand V., le Meuth V., Guilloteau P., Vaysse N., Fourmy D.;

"Molecular cloning, developmental expression and pharmacological

characterization of the CCKB/gastrin receptor in the calf pancreas.";

Eur. J. Pharmacol. 297:165-179(1996).

-I- FUNTION: Receptor for gastrin and cholecystokinin. The CKK-B

receptors occur throughout the central nervous system where they

modulate anxiety, analgesia, arousal, and neuroleptic activity.

This receptor mediates its action by association with G proteins

that activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, mammalia, Eutenestomi, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos. MCBI_TaxID=9913,
                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
S-palmitoyl cysteine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
                                                                                                                                                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYLORIASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                      Score 98.5; DB 1; Leus-...
Pred. No. 0.0033;
Tred. No. 2.09; Indels 27;
                                                       PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
                                                                                                                                                                                      4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                         2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              POLY-LEU.
006D811A6AA065C6 CRC64;
                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 L-PRSRLEMITLITPIPGPVPGPRPNQ--AKLLAKKRVVR 338
                                                                                                                   1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 TRPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 AA
                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             2 ELYQGIKFEASQKKSAKER------
         PIR; A46195; A46195.
Interpro; IPR000276; GPCR_Rhodpsn.
PFam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P79266;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                       48956 MW;
                                                                                                                                                                                                                                                                                                                                                                               25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                      30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                       . Query Match
. Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                       452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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TRANSMEM
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TRANSMEM
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ELYQGIKFEASQKKSAKER-----KPSTTSSGKY-------EDSDGCYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37; Gaps
                               -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-palmitoyl cysteine (By similarity) A2846A580508ABA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 42, Last annotation update)
Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
CCKBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 29.2%; Pred. No. 0.0088; Matches 31; Conservative 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 KTRPPRKLELRQLST----GSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein, Palmitate, Phosphorylation.
DOMAIN 1 57 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
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BY SIMILARITY
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CYTOPLASMIC (
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TISSUE-Liver;
MEDLINE-94324990; PubMed=8048969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
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10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                receptor
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                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KPSTTSSGKYEDSDGCYL- 38
Blandizzi C., Song I., Yamada T.; "Molecular cloning and structural analysis of the rabbit gastrin/CCKB
                                                         FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity. This receptor mediates its action by association with G proteins
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                                                                                                           receptor mediates its action by association with G proter activate a phosphatidylinositol-calcium second messenger
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E0716FCCIDB38870 CRC64;
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91.5; DB 1; Length 452;
Pred. No. 0.018;
5; Mismatches 27; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PSS0262, G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                     SÚBCELLULAR LOCATION: Integral membrane protein.
                                              Biophys. Res. Commun. 202:947-953(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GASR_CANFA STANDARD; PRT; 453 AA P3.0455; 046376; 01-ARR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update)
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EMBL, L31547; AAA31194.1; JOINED.
PIR: JC2459; JC2459.
HSSP; P02699; 1F88.
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PRINTS; PR00237; GPCRRHODOPSN
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AC P30552
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DT 01-APR
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                                                                                                                                                                                                                                                                                                               Song I., Blandizzi C., Brown D.R., Kang D.H., Todisco A., Delvalle J., del Tacca M., Owyang C., Yamada T.;
"Molecular cloning and structural analysis of the canine gastrin/CCK-B
                                                                                                                                                                                         Kopin A.S., Lee Y.-M., McBride E.W., Miller L.J., Lu M., Lin H.Y., Kolakowski L.F. Jr., Beinborn M.; "Expression cloning and characterization of the canine parietal cell
                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for gastrin and cholecystokinin. The CKK-B receptors occur throughout the central nervous system where they modulate anxiety, analgesia, arousal, and neuroleptic activity. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- TISSUE SPECIFICITY: Parietal cells, pancreas, brain and various neoplastic tissues.
-:- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                              Canis familiaris (Dog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
S-palmitoyl cysteine (By similarity)
                Gastrin/cholecystokinin type B receptor (CCK-B receptor) (CCK-BR)
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N-LINKED (GLCNAC. .) (FOTENTIAL)

N-LINKED (GLCNAC. .) (FOTENTIAL)

N-LINKED (GLCNAC. .) (FOTENTIAL)
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein; Palmitate; Phosphorylation.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 89:3605-3609(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL).
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Parietal cell;
MEDLINE-92228835; PubMed=1373504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AD001537; AAB87706.1; -. PIR; S32817; S32817.
HSSP; P02699; 1F88.
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131
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                                                                                                                                                     ----KPSTISSGKYEDSDGCYLK-T 40
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=99365256; PubMed=10433561;
Villard L., Fontes M., Ewbank J.J.;
"Characterization of xnp-1, a Caenorhabditis elegans gene similar to the human XNP/ATR-X gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                   ATRX CAEEL STANDARD; PRT; 1359 AA.
09U7E0; 002061;
28-FEB-2003 (Rel. 41, Created)
15-MAR-2004 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transcriptional regulator ATRX homolog (X-linked nuclear protein-1).
XNP-1 OR B0041.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Bristol N2;
Fulton R., Wohldmann P.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Could be a global transcriptional regulator. Modifies gene expression by affecting chromatin (Potential).
-!- SUBCELLUTAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
                                                                                    25;
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DNA repair; Hydrolase; Helicase; Nuclear protein; ATP-binding;
DNA-binding.
                                    21.9%; Score 85.5; DB 1; Length 453; 28.3%; Pred. No. 0.08; ive 14; Mismatches 32; Indels 2!
453 AA; 48518 MW; 0FAEB7B994B44E1F CRC64;
                                                                                                                                                                                                                                               303 KSROTLELSALTAPTPGPGGGPRPYQ--AKLLAKKRVVR 339
                                                                                                                                                                                                           79
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WormPep; B0041.7; CE17314.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase C.
InterPro; IPR00030; SNF2_N.
Pfam; PF00271; helicase C; 1.
Sfam; PF00176; SNF2_N; I.
SNAART; SN00487; DEXDC; 1.
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                                                                               28; Conservative
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639
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272
281
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                                    Query Match
Best Local Similarity
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SEQUENCE
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J. Biol. Chem. 265:3012-3016(1990).
-!- FUNCTION: Pancreastatin strongly inhibits glucose induced insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sequence of porcine chromogranin A messenger RNA demonstrates chromogranin A can serve as the precursor for the biologically active
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93345362; PubMed=8344192;
Fasciotto B.H., Trauss C.A., Greeley G.H., Cohn D.V.;
"Parastatin (porcine chromogranin A347-418), a novel chromogranin A-derived peptide, inhibits parathyroid cell secretion.";
Endocrinology 133:461-466(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-1987 (Rel. 04, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Chromogranin A precursor (CgA) [Contains: Pancreastatin; Parastatin;
WE-14] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Parastatin inhibits low calcium-stimulated parathyroid cell secretion.
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PTM: O-glycosylated.
PTW: Parathyroid CHGA is sulfated on tyrosine residues, whereas adrenal CHGA seems to be mainly sulfated on oligosaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88196011; PubMed=2834189;
Iacangelo A.L., Fischer-Colbrie R., Koller K.J., Brownstein M.J.,
Eiden L.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Pancreastatin, a novel pancreatic peptide that inhibits insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Neuroendocrine and endocrine secretory
                                                                                                                                                                                                                4
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Gorr S.U., Cohn D.V.;
"Secretion of sulfated and nonsulfated forms of parathyroid
                                                                                                                                                   DB 1; Length 1359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87065127; PubMed=3537810;
Tatemoto K., Efendie S., Mutt V., Makk G., Feistner G.J.,
Barchas J.D.;
                                                                                                                                                                                                             34; Indels
                                                          479 479 C -> F (IN REF. 2).
1359 AA; 156191 MW; BB4342547D4F4E64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 AA
                                                                                                                                                                                                          12; Mismatches
                                                                                                                                                18.7%; Score 73; 31.5%; Pred. No.
POLY-LYS.
POLY-LYS.
C -> F (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endocrinology 122:2339-2341(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          release from the pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                              167 KSKKNKEKSVKKR 179
                                                                                                                                                                                                                                                                                                                                                                                      64 SNSSAANLMAKKR 76
                                                                                                                                                                                                          23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 324:476-478(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreastatin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
   608
862
479
                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 256-304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 363-377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secretion.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
MISCELLANEOUS: Binds calcium with a low-affinity.
SIMILARITY: Belongs to the chromogranin / secretogranin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PĀRĀSTATIN.
BY SINTLARITY.
ANIDATION (G-305 PROVIDE AMIDE GROUP).
D9801P9596D39CD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                              Signal; Amidation; Glycoprotein; Sulfation; Calcium-binding.
NON TER 1 1 1 SIGNAL <1 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.3%; Score 71.5; DB 1; Length 446; 32.5%; Pred. No. 2.5;
                                                                                                                                  and
                                                                                                                use by non-profit institutions as long as its cont modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOGRANIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 2.5;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                PANCREASTATIN.
WE-14.
                                                                                                                                                                                                                              HSSP; PO5059; ICFK.
GlycosuiteDB; P04404; -.
Interpro; IPR001919; Chromogranin_AB.
InterPro; IPR001990; Granin.
Pfam; PF01271; Granin; 1.
PRINTS; PR00659; CHROMOGRANIN.
PROSITE; PS00422; GRANINS 1; 1.
PROSITE; PS00423; GRANINS 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49323 MW;
                                                                                                                                                                                                EMBL; M20926; AAA31016.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.3
Best Local Similarity 32.5
Matches 25; Conservative
                                                                                                                                                                                                               , A32284; A32284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 AA;
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MOD RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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Search completed: October 1, 2004, 16:36:59 Job time: 11 secs

| |:|:||| 173 ----STHPLASLPSKKR 185

셤

60 NRIRSNSSAANLMAKKR 76

g

2 ELYQGIKFEASQKKSAKERKPSTTSSGKYEDSDGC--YLKTRPPRKLELRQLSTGSSSRA 59

7; Gaps

35; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 1, 2004, 16:34:09; Search time 39 Seconds (without alignments) 639.127 Million cell updates/sec

US-09-841-091B-20 391 1 LELYQGIKFEASQKKSAKER.....NRIRSNSSAANLMAKKRVIR 79 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 segs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organele:*
sp_organele:* SPTREMBL 25:* Database :

plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_rvirus:*
sp_bacteriap:*
sp_archeap:* : 10

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	nlnosnm snm 9xqp60	OBvcc7 mus musculu	O7tlD8 gallus gall	Ogubvi homo sapien	075824 homo sapien	Q92492 homo sapien	homod	Q8bkf6 mus musculu	Р90333 ргаомув пас	P89000 praomys nat	P89005 praomys nat	Q63095 rattue norv	Q9nyk7 homo sapien	Q961c6 homo sapien	Q933q6 shiqella fl	
	ID	Q9DBV6	Q8VCC7	Q7T1P8	Q9UBV1	075824	092492	Q16144	QBBKF6	P90333	P89000	P89005	Q63095	Q9NYK7	921960	93306	090602
	DB	1	11	13	4	4	4	4	11	1	1	11	11	4	4	0	Ŋ
	Query Match Length DB	436	436	436	90	396	396	447	453	296	316	450	381	516	516	258	225
æ	Query Match	72.8	72.8	35.4	28.6	28.6	28.6	28.6	26.3	26.0	26.0	26.0	25.2	23.7	23.7	20.8	18.9
	Score	284.5	284.5	138.5	112	112	112	112	103	101.5	101.5	101.5	98.5	92.5	92.5	81.5	74
	Result No.	п	~	m	4	S	9	7	α	σ	10	11	12	13	14	15	16

07yuds drosophila	Q7yud4 drosophila		Q8mvnl boltenia vi	P91959 psammechinu	045614 caenorhabdi	Q9xyh9 leishmania	Q984j4 streptococc	09x6g6 streptococc	Q9x9c0 streptococc	Q8nix6 neurospora	Q9d029 mus musculu	O14562 homo sapien	O9nkyl drosophila	Q868m6 dugesia jap	Q9le81 arabidopsis	Q9fwv2 oryza sativ	Q7xd45 oryza sativ	Q28708 oryctolagus	Q9nah6 caenorhabdi	Q8eyk4 leptospira		Q9vj42 drosophila	Q8r185 mus musculu	Q8bka3 mus musculu		O9w0h4 drosophila	Q18264 caenorhabdi	Q8utv3 human immun
Q7YUDS	Q7YUD4	Q8IG74	QBMVN1	P91959	045614	6НХХ6О	Q9S4J4	959x60	036X6Q	OBNIX6	1 090029	014562	Q9NKY1	Q868M6	0 Q9LE81	0 Q9FWV2	0 Q7XD45	028708	Q9NAH6	6 Q8EYK4	Q861Y3	Q9VJ42	1 Q8R1S5	1 Q8BKA3	0 Q9ZWB1	Q9W0H4	Q18264	5 Q8UTV3
225 5	225 5	585 5	213 5	299 5	3102 5	91 5	229 2	246 2	435 2	204 3	309 1	533 4	1045 5	1076 5	1168 1	988 1	988	533 6	580 5	695 1	509 5	1377 5	120 1	608	672 1	1150 5	1715 5	134 1
18.9	18.9	18.7	18.3	18.3	18.3	18.2	18.2	18.2	18.2	18.0	18.0	18.0	18.0	17.9	17.9	17.8	17.8	17.5	17.5	17.5	17.4	17.4	17.3	17.3	17.3	17.3	17.3	17.1
74	74	73	71.5	71.5	71.5	71	71	71	71	70.5	70.5	70.5	70.5	70	70	69.5	69.5	68.5	68.5	68.5	68	68	67.5	67.5	67.5	67.5	67.5	67
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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varatora, yaratora, varatora,, oraniata; Vertebrata; Euteleostomi; Bukaryota; Ares; Neognathae; Galliformes; Phasianidae; Phasianinae; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                   Nilsson I.B.M., Monstein H.J., Svensson S.P.S.; "Molecular cloning and characterization of a chicken brain cholecystokinin receptor.";
                                                                                                                                                                                                                                                                                                                                                                TISSUE-Brain;
Nilsson I.B.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AJ489483; CAD33800.1; -.
                                                                                                                                                                                                                                                                                                           Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RIRSNSSAANLMAKKRVIR 79
                                                                         Cholecystokinin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                           Gallus gallus (Chicken)
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UBV1;
01-MAY-2000 (
01-MAY-2000 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                   Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UBV1
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020534; AAH20534.1;
MGD; MGI:99478; Cckar.
GG; GG:0016621; C:integral to membrane; IEA.
GG; GG:0004872; F:receptor activity; IEA.
GG; GG:0001884; F:rhodopsin-like receptor activity; IEA.
GG; GG:000186; P:G-protein coupled receptor protein signalin. .; IEA.
PF00001; TPR000275; GFCR_Rhodpsn.
PF00001; 7tm 1; 1.
PRINTS; PR00237; GFCRRHODOPSN.
                                                                                                                                                                                                                                                                                                25
HSSP; P02699; 1F88.

Which, Mail: 99478; Cckar.

GO; GO:0016021; Crintegral to membrane; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001386; P:C-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PP00001; 7tm_1; I.

PROSITE; PS00237; GPROTEIN_RECEP_F11; 1.

PROSITE; PS00237; GPROTEIN_RECEP_F12; I.

SEQUENCE 436 AA; 48446 MW; 49B4AD57F080F08A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LELYQGIKFEASOKKSAKERKPST-----TSSGKYEDSDGCYL-KTRPPRKLELRQLS
                                                                                                                                                                                                                                                                                            1 LELYQGIKFEASQKKSAKERKPST-----TSSGKYEDSDGCYL-KTRPPRKLELRQLS
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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ق
                                                                                                                                                                                                                     72.8%; Score 284.5; DB 11; Length 436; 71.6%; Pred. No. 1.5e-24; ive 10; Mismatches 6; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.8%; Score 284.5; DB 11; Length 436;
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Pred. No. 1.5e-24;
"'-matches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 AA; 48396 MW; FD35D8453B792F79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 TSSSGGRINRIRSSGSAANLIAKKRVIR 321
                                                                                                                                                                                                                                                                                                                                                                                        294 TSSSGGRINRIRSSGSAANLIAKKRVIR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 TGSS-SRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                                                                                                                                                      53 TGSS-SRANRIRSNSSAANLMAKKRVIR 79
                                                                                                                                                                                                                                         71.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VCC7;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2003 (TrEMBLrel. 24,
Cholecystokinin A receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.63
Matches 63; Conservative
                                                                                                                                                                                                                                                            63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
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                                                                                                                                                                                                                          Query Match
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Q7T1P8
ID Q7T1P8
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QBVCC7

qq

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CCKAR

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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDIJIBE-94036800; PubMed=8221657;
MEDIJIBE-94036800; PubMed=8221657;
Sethi T., Herget T., Wu S.V., Walsh J.H., Rozengurt E.;
"CCKA and CCKB receptors are expressed in small cell lung cancer lines and mediate Ca2+ mobilization and clonal growth.";
Cancer Res. 53:5208-5213(1993).
SEQUENCE 90 AA; 9547 MW; 336A0F09E7C0857B CRC64;
                                                                                                                                                                                                            2 ELYQGIKPEASQKKSAKERKPSTTSSGKYEDSDGCYLK-TRPPRKLELRQLSTGSSSRAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ELYQCIKFEASQKKSAKER----KTR---KPSTTSSGKYEDSDGCYL---KTR
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28.6%; Score 112; DB 4; Length 90;
Best Local Similarity 33.7%; Pred. No. 2.4e-05;
Matches 34; Conservative 14; Mismatches 19; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Cholecystokinin B/gastrin receptor (Fragment).
Cholecystokinin B/gastrin receptor (Fragment).
Eukaryota, Metakuman).
Eukaryota, Metakuman).
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                   DB 13; Length 436;
                                                               'Match 35.4%; Score 138.5; DB 13; Length Local Similarity 45.6%; Pred. No. 1.2e-07; les 36; Conservative 13; Mismatches 27; Indels
436 AA; 47749 MW; 429C1D7AFE774DC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 P--ALELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR
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436 AA

PRELIMINARY;

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J. Biol. Chem. 268:18300-18305(1993).
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 16-26 FROM N.A.
MEDLINE=95194412; Pubmed=7887934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholecystokinin B receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; 165231, 165231.
HSSP; P02699; 1F88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                               SEQUENCE FROM N.A.
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                              Miyake A.;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
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MEDLINE=93352657; PubMed=8349705;
Ito M., Matzui T., Taniguchi T., Tsukamoto T., Murayama T., Arima N.,
Nakata H., Chiba T., Chibara K.;
"Functional characterization of a human brain cholecystokinin-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cholecystokinin-B receptor/gastrin receptor (CCK-B gastrin receptor
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    MEDLINE=99087707; PubMed=9872672;
0'Briant K.C., Ali S.Y., Weier H.U.G., Bepler G.;
"An 84-kilobase physical map and repeat polymorphisms of the gastrin/cholecystokinin brain receptor region at the junction of chromosome segments 11p15.4 and 15.5.";
chromosome Res. 6.415-418(1998).
EMBL; AF074029; AAC27510.1;
EMBL; AF074029; AAC27510.1;
PIR; 165231; 165231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional characterization of a human brain cholecystokinin-B receptor. A trophic effect of cholecystokinin and gastrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                     PLN, GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; F:rhodopsin-like receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodopsn.
Pfam; PR0001, 7tm 1; 1.
PRINTS; PR00237; GFCRHODOPSN.
PROSITE; PS000237; GFCRHODOPSN.
PROSITE; PS000237; GFRHODOPSN.
PROSITE; PS000237; GFRHODOPSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 AA; 43286 MW; 54BE9A8D0257C4E5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPRKLELRQLST---GSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Gastrin\cholecystokinin brain receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 112; DB 4;
Pred. No. 0.00012;
                                                   396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Conservative 14; Mismatches
                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.6%;
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                                                   PRELIMINARY;
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CCKBR OR CCK-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                     Homo sapiens (Human)
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NON TER
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                                                 075824
                                                                                                                                                       CCKBR.
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RESULT (922492 AC 0937 AC 0937

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193 BLYLGLRFDGDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVG--EDSDGCYVQLPRSR 250
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GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001386; F:rhodopsin-like receptor protein signalin. .; IEA.
GO; GO:0001386; F:G-protein coupled receptor protein signalin. .; IEA.
InterPro; IPRO00276; GPCR.Rhodpsn.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1_2; 1.
NON_TER 396
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MEDLINE=95151631; PubMed=7848914;
MEDLINE=951516131; PubMed=7848914;
ItO M., Iwata N., Taniguchi T., Murayama T., Chihara K., Matsui T.;
"Functional characterization of two cholecystokinin-B/gastrin receptor
"Functional characterization of two cholecystokinin-B/gastrin receptor
isoforms: a preferential splice donor site in the human receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ELYQGIKFEASQKKSAKER-----KPSTTSSGKYEDSDGCYL--KTR
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TISSUE=Brain;
MEDLINE=94241526; PubMed=8185170;
Herget T., Sethi T., Wu S.V., Walsh J.H., Rozengurt E.;
Herget T., Stockin stimulates Ca2+ mobilization and clonal growth in small cell lung cancer through CCKA and CCKB/gastrin receptors.";
                                                                                                           gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'A truncated isoform of human CCK-B/gastrin receptor generated by
TISSUE-Lung;
MEDLINE=94038108; PubMed=8222757;
Zimonjic D.B., Popescu N.C., Matsui T., Ito M., Chihara K.;
Zimonjic D.B., Popescu N.C., Matsui T., Ito M., Chihara K.;
Localization of the human cholecystokinin-B/gastrin receptor concerning to chromosome lipl5.5-->pl5.4 by fluorescence in situ hybridization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 AA; 43252 MW; A25DD5597CA903C0 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alternative usage of a novel exon.";
Blochem. Blophys. Res. Commun. 208:230-237(1995).
EMBL; D21219; BAA04759.1; -.
EMBL; S76072; AAB33740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%; Score 112; DB 4; 33.7%; Pred. No. 0.00012;
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Best Local Similarity 33.7%; Pred. No. v.v.
Matches 34; Conservative 14; Mismatches
                                                                                                                                                                                                                  /togenet. Cell Genet. 65:184-185(1994)
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302 QL-PRSRLEMITLITPTIGPGPGPRPNQ--AKLLAKKRVVR 339
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PRINTS; PR00237; GPCRRHODOPSN
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                                                                   PRELIMINARY;
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Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                            Mastomys.
NCBI_TaxID=10112;
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01-MAY-1997 (
01-JUN-2003 (
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SEQUENCE
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P90333;
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P89000
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P90333
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                                                                                                                                                                                                                                                                                                   244 ELYLGLRFDGDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGK--DSDGCYVQLPRSR 301
                                                   GO, GO:0016021, C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR_Rhodopsn.
PFam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                            41
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Mature 420:563-573 (2002).

EMBL, AK053307; BAC35337.1; -.

EMBL, AK053307; BAC35337.1; -.

EMBL, AK053307; Calibre accident to membrane; IEA.

GO; GO:001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.

FRO00276; FRO00276; FROM Rhodopsn.

PFRO001; 7tm_1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                          2 ELYQGIKFEASOKKSAKER-----KPSTTSSGKYEDSDGCYL---KTR
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                               34;
                                                                                                                                                                                                                   Match 28.6%; Score 112; DB 4; Length 447; Local Similarity 33.7%; Pred. No. 0.00014; les 34; Conservative 14; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length, 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.3%; Score 103; DB 11; Length 4 29.7%; Pred. No. 0.0016; ive 16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP FI_1; 1.
SEQUENCE PS0262; GPROTEIN_RECEP FI_2; 1.
SEQUENCE 453 AA; 49143 MW; FCE07980A678250A CRC64;
                                                                                                                                                                                                                                                                                                                                                  302 P--ALELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 333
                                                                                                                                                                                         447 AA; 48418 MW; E3DAAE5EE1F0FB99 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Gastrin/cholecystokinin type B receptor.
                                                                                                                                                                                                                                                                                                                               PPRKLELRQLST---GSSSRANRIRSNSSAANLMAKKRVIR
                                                                                                                                                                                                                                                                                                                                                                                                                             453 AA
                                                                                                                   PEam; PF00001; 7tm 1, 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
713:283-297 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Eye;
MEDLINE=22354683; PubMed=12466851;
         EMBL, S70057, AAB30766.2; -. PIR, 165231, 165231.
HSSP, P02699; 1F88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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01-OCT-2003
                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                      Query Match
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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The Aracins natalensis (African soft-furred rat) (Mastomys natalensis).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
61-UNY-2003 (TrEMBLrel. 24, Last annotation update)
62strin/cholecystokinin receptor (Fragment).
62strin/cholecystokinin receptor fragment).
62strin/cholecystokinin receptor fragment).
63strin/cholecystokinin receptor fragment).
64strican soft-furred rat) (Mastomys natalensis)
65strican soft-furred rat) (Mastomys natalensis)
65strican soft-furred rat) (Mastomys natalensis)
65strican soft-furred rat)
65strican soft-furr
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:-protein compled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Luque E.A., Tang L.H., Modlin I.M.;
"Gastrin receptors in Mastomys natalensis.";
Submitted (FEB-1996 to the EMBL/GenBank/DDBJ databases.
EMBL; U49833; AB41676.1; -.
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296 296 296 MW; 320FF55B102DB4C2 CRC64;
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(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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"Gastrin Receptors in Mastomys Natalensis.";
Gastroenterology 0:0-0(0).
EMBL; U48614; AAB41829.1; -.
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CCK(B) receptor (CCK2 receptor) (Fragment).
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                                                                                                                                                    244 ELYLGLRFDGDNDSDTQSRVRNQGGLPGGTAPGPVHQNGGCRHVTVAGEDNDGCYVQL-P 302
                                                                                                                                     2 ELYQGIKFEASQKKSAKER-----KPSTISSGKY------EDSDGCYLKTRP 42
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; F:G-protein coupled receptor protein signalin. . ; IEA.
InterPro; IPR000276; GPCR Rhodpsn.
PFem; PF00001; 7tm 1; 1.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Gastrin/cholecystokinin-B receptor (Fragment).
Pracmys natalensis (African soft-furred rat) (Mastomys natalensis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                           Length 316;
                                                                                                                 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Luque E.A., Tang L.H., Modlin I.M., "Gastrin receptor expression in Mastomys natalensis."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                            1 1
316 316
316 AA: 34726 MW; F0D346BAFC6C19E6 CRC64;
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Last sequence update)
Last annotation update)
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303 RSRLEMTTLTTPTPGFG---LASANQAKLLAKKRVVR 336
                                                                                           DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 PRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIR 79
                                                                                        26.0%; Score 101.5; DB : 28.9%; Pred. No. 0.0016; Live 18; Mismatches 2
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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28; Conservative
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                                                                                          Query Match
Best Local Similarity
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Q63095
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"Genetic variations in CCK2 receptor in PvG hooded and Sprague-Dawley rats and its mRNA expression on cat exposure.";

In Behav. Neurosci. 117:385-390(2003).

EMBL; X79209; CAA55798.1; -.

REMBL; X79209; CAA55798.1; -.

REMBL; AX303996; AAP59041.1; -.

REMBL; AX303996; AAP590021. Cintegral to membrane; IEA.

GO; GO:0001894; Fireceptor activity; IEA.

GO; GO:0001894; Fireceptor activity; IEA.

RO; GO:0001894; Fireceptor activity; IEA.

RO; GO:0007186; P:G-protein coupled receptor protein signalin. ..; IEA.

REMINS; PRO0031; GPROTEIN RECEP 11; 1.

REMOSITE; PSS00237; G-PROTEIN_RECEP 11; 1.
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                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
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                                                                                                                                                                                              MEDLINE=95016646; PubMed=7931273;
Jagerschmidt A., Popovici T., O'Donohue M., Roques B.P.;
"Identification and characterization of various cholecystokinin B receptor mRNA forms in rat brain tissue and partial determination the cholecystokin B receptor gene structure.";
J. Neurochem. 63:1199-1206(1994).
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Hellmich M.R., Rui X.L., Hellmich H.L., Fleming R.Y.D., Evers B.M. Tromsend C.M. Jr.
Tromsend C.M. Jr.
"Human Colorectal."
"Human Colorectal."
"A Bool. Chem. Tromsend Colorectal."
"Bool. Chem. 275:32122-33128 (2000).
EMBL; AF239668; AAF67174.1; --
PIR; 165231; 165231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22594138; PubMed=12708535;
Wang H., Zhu Y.Z., Farook J.M., Moochhala S., Teo A.L., Lee L.K.,
Wong P.T.;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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381 AA; 41667 MW; DDCB40806A604A4D CRC64;
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Best Local Similarity 30.0%; Pred. No. 0.00
Matches 30; Conservative 14; Mismatches
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Rattus norvegicus (Rat)
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21 KPSTTSSGKYEDSDGCYL---KTRPPRKLELRQLST---GSSSRANRIRSNSSAANLMAK
                                                                                   / Match 23.7%; Score 92.5; DB 4; Length 516; Local Similarity 43.1%; Pred. No. 0.03; nes 28; Conservative 9; Mismatches 11; Indels 1
516 AA; 55841 MW; EC7EB8505C9A8F0D CRC64;
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EMBL; AY029770; AAK38151.1; -

EMBL; AF441129; AAN32829.1; -

REMBL; AF441129; ARN32829.1; -

REMBL; AF441129; AF47129; Fireceptor activity; IEA.

GO; GO:000186; P:rhodopsin-like receptor activity; IEA.

GO; GO:000186; P:rhodopsin-like receptor protein signalin. .; IEA.

RO; GO:0001186; P:Rhodopsin-like receptor protein signalin. .; IEA.

REMBL; PRO0001; 7rum 1; 1.

REMBL; PRO00237; GPRRHODOPSN.

RECEPTE; PSO0237; G-RROTEIN_RECEP_F1_1; 1.

RECEPTOR:

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R GO; GO: 0004951; F: cholecystckinin receptor activity; ISS.
R GO; GO: 0004951; F: phosphatidylinositol 3-kinase regulator act. . .; ISS.
R GO; GO: 0004835; F: phosphoinositide phospholipase C activity; ISS.
R GO; GO: 0007204; P: cytosolic calcium ion concentration elevation; ISS.
R GO; GO: 0007204; P: cytosolic calcium ion concentration elevation; ISS.
R GO; GO: 0007301; P: feeding behavior; ISS.
R GO; GO: 0007301; P: phospholipase C activation; ISS.
R GO; GO: 0007631; P: phospholipase C activation; ISS.
R GO; GO: 0007601; P: sensory perception; ISS.
R GO; GO: 0007601; TSR GO; RR Rhodpsn.
R PRINTS; PRO0021; GFCRRHODOPSN.
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                                                                                                                                     .; ISS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=22216923; PubMed=12429993;
Smith J.P., Verderame M.F., McLaughlin P., Martenis M., Ballard
Zagon I.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92.5; DB 4; Length 516;
Pred. No. 0.03;
9; Mismatches 11; Indels 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CCK-B/gastrin receptor variant (Cholecystokinin-C receptor).
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Submitted (APR-2001) to the BMBL/GenBank/DDBJ databases
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SEQUENCE
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10261CG
1026
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"The Iron- and Temperature-Regulated cjrBC Genes of Shigella and Entercinvasive Escherichia coli Strains Code for Colicin Js Uptake.";
J. Bacteriol. 183:3958-3966 (2001).
EMBL; AF281292; AAK67308-1; -..
EMBL; AF281291; AAK67308-1; -..
EMBL; AF281291; AAK67308-1; -..
EMBL; AF281291; CABC Company Cterm; J. SEQUENCE 258 AA; 28689 WW; 55A5504B909C32DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EASQKKSAKERKPSTTSSG-----KYEDSDGCYLKTRPPRKLELRQLSTGSSSRANRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Gaps
                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=623, 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.8%; Score 81.5; DB 2; Length 258; 29.3%; Pred. No. 0.26; ive 14; Mismatches 28; Indels 1:
                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                              258 AA
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                                                                                                                                                                                 Created)
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SPECIES-S.flexneri, and E.coli;
MEDLINE-21289081; PubMed=11395459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 SSNAAPQALVESSRI 148
                                                                                                                                                                            (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smajs D., Weinstock G.M.;
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                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                          Shigella flexneri, and Escherichia coli.
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Best Local Similarity
398 KRVVR 402
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